

SEQUENCE LISTING

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<120> Method for Zymotic Production of Fine Chemicals Containing
 Sulphur (metY)

<130> 13111-00006-US

<150> PCT/EP 2003/009453
 <151> 2003-08-26

<150> DE 102 39 082.7
 <151> 2002-08-26

<160> 79

<170> PatentIn version 3.3

<210> 1

<211> 1317

<212> DNA

<213> Corynebacterium diphtheriae

<220>

<221> CDS

<222> (1) .. (1317)

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act cgc tcc atc cac gca gga caa agc gtc gat agt gat acc agt gcc	96
Thr Arg Ser Ile His Ala Gly Gln Ser Val Asp Ser Asp Thr Ser Ala	
20 25 30	
cgc aac cta ccg att tac ctg aca tca tcg tac gtt ttt aat gac gcc	144
Arg Asn Leu Pro Ile Tyr Leu Thr Ser Ser Tyr Val Phe Asn Asp Ala	
35 40 45	
gaa cac gca gca aac cgc ttc aac ctt tcc gac gcc ggc ccg gtt tac	192
Glu His Ala Ala Asn Arg Phe Asn Leu Ser Asp Ala Gly Pro Val Tyr	
50 55 60	

tct cgc ctg acc aac cca act gtc gcg gca gtc gaa gaa cgc cta gcc Ser Arg Leu Thr Asn Pro Thr Val Ala Ala Val Glu Glu Arg Leu Ala 65 70 75 80	240
aat ctt gaa ggt ggc gta cac gcc gta ctt ttc gct tcc gga atg gcc Asn Leu Glu Gly Gly Val His Ala Val Leu Phe Ala Ser Gly Met Ala 85 90 95	288
gcc gaa acc gcc gca atc ctc aac atc gcc cgc gcg ggt tcc cac atc Ala Glu Thr Ala Ala Ile Leu Asn Ile Ala Arg Ala Gly Ser His Ile 100 105 110	336
gtg tcc agt cct cgc att tac ggc ggc acc gaa aca ctc ttt gcc gtc Val Ser Ser Pro Arg Ile Tyr Gly Gly Thr Glu Thr Leu Phe Ala Val 115 120 125	384
aca ttg gca cgc ctg ggc atc gaa acc act ttc gta gaa aat cct gac Thr Leu Ala Arg Leu Gly Ile Glu Thr Thr Phe Val Glu Asn Pro Asp 130 135 140	432
gac cca gcc tca tgg gag gct gca gtt caa gac aac acg gta gct ctc Asp Pro Ala Ser Trp Glu Ala Ala Val Gln Asp Asn Thr Val Ala Leu 145 150 155 160	480
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gca atc gca gag gtt gcc cat aaa cat caa gta cca ctg atc gtc gac Ala Ile Ala Glu Val Ala His Lys His Gln Val Pro Leu Ile Val Asp 180 185 190	576
aac acc ctc gca acc gca gcc ctt gta cgc ccc ctc gaa ctc ggt gca Asn Thr Leu Ala Thr Ala Ala Leu Val Arg Pro Leu Glu Leu Gly Ala 195 200 205	624
gac gtc gtc gtg gca tcc cta acc aag ttc tac acc gga aat ggc tcc Asp Val Val Val Ala Ser Leu Thr Lys Phe Tyr Thr Gly Asn Gly Ser 210 215 220	672
gga ctc ggc gga gtg ctt atc gac ggc gga aac ttc gac tgg acc gtc Gly Leu Gly Gly Val Leu Ile Asp Gly Gly Asn Phe Asp Trp Thr Val 225 230 235 240	720
aca cgc aac ggc gaa ccg atc ttc ccc gac ttt gtc acc cca gat ccc Thr Arg Asn Gly Glu Pro Ile Phe Pro Asp Phe Val Thr Pro Asp Pro 245 250 255	768
gcc tat cac ggt ctc aag tat tcc gat ctt ggt gcc ccc gcc ttc gga Ala Tyr His Gly Leu Lys Tyr Ser Asp Leu Gly Ala Pro Ala Phe Gly 260 265 270	816
cta aag gct cgc gtc gga ctc ctg cgc gac acc ggc gca gcc cca tca Leu Lys Ala Arg Val Gly Leu Leu Arg Asp Thr Gly Ala Ala Pro Ser 275 280 285	864
cca ctc aac gca tgg atc acc gca caa ggg ctc gac acc ctc tcg cta Pro Leu Asn Ala Trp Ile Thr Ala Gln Gly Leu Asp Thr Leu Ser Leu 290 295 300	912

cga gta caa cgc cac aac gaa aac gca ctc gca gta gca caa ttc ctc 960
 Arg Val Gln Arg His Asn Glu Asn Ala Leu Ala Val Ala Gln Phe Leu
 305 310 315 320

gcc aac cac gag aaa gta gcc aag gtt aac tac gca ggc ctt ccc gac 1008
 Ala Asn His Glu Lys Val Ala Lys Val Asn Tyr Ala Gly Leu Pro Asp
 325 330 335

tcc cct tgg tac cca gtc aaa gaa aaa ctc gga ttc gac tac acc ggc 1056
 Ser Pro Trp Tyr Pro Val Lys Glu Lys Leu Gly Phe Asp Tyr Thr Gly
 340 345 350

tcc gta ctt tcc ttt gac gtt aaa ggt gga aaa aac gaa gca tgg cgc 1104
 Ser Val Leu Ser Phe Asp Val Lys Gly Gly Lys Asn Glu Ala Trp Arg
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ttt atc gac gca ctc aaa cta cac tcg aac ctc gcc aac gtc gga gac 1152
 Phe Ile Asp Ala Leu Lys Leu His Ser Asn Leu Ala Asn Val Gly Asp
 370 375 380

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 385 390 395 400

gaa gaa tcg gca ctt cta gcc gca gga att aat caa gca acc atc cga 1248
 Glu Glu Ser Ala Leu Leu Ala Ala Gly Ile Asn Gln Ala Thr Ile Arg
 405 410 415

ctc tcc gtc ggc atc gaa tcc atc gac gac atc atc gcc gac ctc aca 1296
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 420 425 430

gca ggt ttc gac gca atc taa 1317
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<212> PRT

<213> Corynebacterium diphtheriae

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 20 25 30

Arg Asn Leu Pro Ile Tyr Leu Thr Ser Ser Tyr Val Phe Asn Asp Ala
 35 40 45

Glu His Ala Ala Asn Arg Phe Asn Leu Ser Asp Ala Gly Pro Val Tyr
 50 55 60

Ser Arg Leu Thr Asn Pro Thr Val Ala Ala Val Glu Glu Arg Leu Ala
 65 70 75 80

Asn Leu Glu Gly Gly Val His Ala Val Leu Phe Ala Ser Gly Met Ala
 85 90 95

Ala Glu Thr Ala Ala Ile Leu Asn Ile Ala Arg Ala Gly Ser His Ile
 100 105 110

Val Ser Ser Pro Arg Ile Tyr Gly Gly Thr Glu Thr Leu Phe Ala Val
 115 120 125

Thr Leu Ala Arg Leu Gly Ile Glu Thr Thr Phe Val Glu Asn Pro Asp
 130 135 140

Asp Pro Ala Ser Trp Glu Ala Ala Val Gln Asp Asn Thr Val Ala Leu
 145 150 155 160

Tyr Gly Glu Thr Phe Ala Asn Pro Gln Ala Asp Val Leu Asp Ile Pro
 165 170 175

Ala Ile Ala Glu Val Ala His Lys His Gln Val Pro Leu Ile Val Asp
 180 185 190

Asn Thr Leu Ala Thr Ala Ala Leu Val Arg Pro Leu Glu Leu Gly Ala
 195 200 205

Asp Val Val Val Ala Ser Leu Thr Lys Phe Tyr Thr Gly Asn Gly Ser
 210 215 220

Gly Leu Gly Gly Val Leu Ile Asp Gly Gly Asn Phe Asp Trp Thr Val
 225 230 235 240

Thr Arg Asn Gly Glu Pro Ile Phe Pro Asp Phe Val Thr Pro Asp Pro
 245 250 255

Ala Tyr His Gly Leu Lys Tyr Ser Asp Leu Gly Ala Pro Ala Phe Gly
 260 265 270

Leu Lys Ala Arg Val Gly Leu Leu Arg Asp Thr Gly Ala Ala Pro Ser
 275 280 285

Pro Leu Asn Ala Trp Ile Thr Ala Gln Gly Leu Asp Thr Leu Ser Leu
 290 295 300

Arg Val Gln Arg His Asn Glu Asn Ala Leu Ala Val Ala Gln Phe Leu
 305 310 315 320

Ala Asn His Glu Lys Val Ala Lys Val Asn Tyr Ala Gly Leu Pro Asp
 325 330 335

Ser Pro Trp Tyr Pro Val Lys Glu Lys Leu Gly Phe Asp Tyr Thr Gly
 340 345 350

Ser Val Leu Ser Phe Asp Val Lys Gly Gly Lys Asn Glu Ala Trp Arg
 355 360 365

Phe Ile Asp Ala Leu Lys Leu His Ser Asn Leu Ala Asn Val Gly Asp
 370 375 380

Val Arg Ser Leu Val Val His Pro Ala Thr Thr Thr His Ser Gln Ser
 385 390 395 400

Glu Glu Ser Ala Leu Leu Ala Ala Gly Ile Asn Gln Ala Thr Ile Arg
 405 410 415

Leu Ser Val Gly Ile Glu Ser Ile Asp Asp Ile Ile Ala Asp Leu Thr
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Ala Gly Phe Asp Ala Ile
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<210> 3

<211> 1350

<212> DNA

<213> Mycobacterium tuberculosis

<220>

<221> CDS

<222> (1)..(1350)

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Ser Phe Glu Thr Lys Gln Ile His Ala Gly Gln His Pro Asp Pro Thr	
20 25 30	
acc aac gcc cgg gct ctg ccg atc tat gcg acc acg tcg tac acc ttc	144
Thr Asn Ala Arg Ala Leu Pro Ile Tyr Ala Thr Thr Ser Tyr Thr Phe	
35 40 45	
gac gac acc gcg cac gcc gcc gcc ctg ttc gga ctg gaa att ccg ggc	192
Asp Asp Thr Ala His Ala Ala Leu Phe Gly Leu Glu Ile Pro Gly	
50 55 60	
aat atc tac acc cgg atc ggc aac ccc acc acc gac gtc gtc gag cag	240
Asn Ile Tyr Thr Arg Ile Gly Asn Pro Thr Thr Asp Val Val Glu Gln	
65 70 75 80	
cgc atc gcc gcg ctc gag ggc ggt gtg gcc gcg ctg ttc ctg tcg tcg	288
Arg Ile Ala Ala Leu Glu Gly Gly Val Ala Ala Leu Phe Leu Ser Ser	
85 90 95	
ggg cag gcc gcg gag acg ttc gcc atc ttg aac ctg gcc ggc gcg ggc	336
Gly Gln Ala Ala Glu Thr Phe Ala Ile Leu Asn Leu Ala Gly Ala Gly	
100 105 110	
gat cac atc gtg tcc agc ccg cgc ctg tac ggc ggc acc tac aac ctg	384
Asp His Ile Val Ser Ser Pro Arg Leu Tyr Gly Gly Thr Tyr Asn Leu	
115 120 125	
ttc cac tat tcg ctg gcc aag ctc ggc atc gag gtc agc ttc gtc gac	432
Phe His Tyr Ser Leu Ala Lys Leu Gly Ile Glu Val Ser Phe Val Asp	
130 135 140	
gat ccg gac gat ctg gac acc tgg cag gcg gcg gta ccg ccc aac acc	480
Asp Pro Asp Asp Leu Asp Thr Trp Gln Ala Ala Val Arg Pro Asn Thr	
145 150 155 160	
aag gcg ttc ttc gcc gag acc atc tcc aac ccg cag atc gac ctg ctg	528
Lys Ala Phe Phe Ala Glu Thr Ile Ser Asn Pro Gln Ile Asp Leu Leu	
165 170 175	
gac acc ccg gcg gtt tcc gag gtc gcc cat cgc aac ggg gtg ccg ttg	576
Asp Thr Pro Ala Val Ser Glu Val Ala His Arg Asn Gly Val Pro Leu	
180 185 190	
atc gtc gac aac acc atc gcc acg cca tac ctg atc caa ccg ttg gcc	624
Ile Val Asp Asn Thr Ile Ala Thr Pro Tyr Leu Ile Gln Pro Leu Ala	
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cag ggc gcc gac atc gtc gtg cat tcg gcc acc aag tac ctg ggc ggc	672
Gln Gly Ala Asp Ile Val Val His Ser Ala Thr Lys Tyr Leu Gly Gly	
210 215 220	
cac ggt gcc gcc atc gcg ggt gtg atc gtc gac ggc ggc aac ttc gat	720
His Gly Ala Ala Ile Ala Gly Val Ile Val Asp Gly Gly Asn Phe Asp	

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Trp Thr Gln Gly Arg Phe Pro Gly Phe Thr Thr Pro Asp Pro Ser Tyr				
	245	250	255	
cac ggc gtg gtg ttc gcc gag ctg ggt cca ccg gcg ttt gcg ctc aaa				816
His Gly Val Val Phe Ala Glu Leu Gly Pro Pro Ala Phe Ala Leu Lys				
	260	265	270	
gct cga gtg cag ctg ctc cgt gac tac ggc tcg gcg gct tcg ccg ttc				864
Ala Arg Val Gln Leu Leu Arg Asp Tyr Gly Ser Ala Ala Ser Pro Phe				
	275	280	285	
aac gcg ttc ttg gtg gcg cag ggt ctg gaa acg ctg agc ctg cgg atc				912
Asn Ala Phe Leu Val Ala Gln Gly Leu Glu Thr Leu Ser Leu Arg Ile				
	290	295	300	
gag cgg cac gtc gcc aac gcg cag cgc gtc gcc gag ttc ctg gcc gcc				960
Glu Arg His Val Ala Asn Ala Gln Arg Val Ala Glu Phe Leu Ala Ala				
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cgc gac gac gtg ctt tcg gtc aac tat gcg ggg ctg ccc tcc tcg ccc				1008
Arg Asp Asp Val Leu Ser Val Asn Tyr Ala Gly Leu Pro Ser Ser Pro				
	325	330	335	
tgg cat gag cgg gcc aag agg ctg gcg ccc aag gga acc ggg gcc gtg				1056
Trp His Glu Arg Ala Lys Arg Leu Ala Pro Lys Gly Thr Gly Ala Val				
	340	345	350	
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Leu Ser Phe Glu Leu Ala Gly Gly Ile Glu Ala Gly Lys Ala Phe Val				
	355	360	365	
aac gcg ttg aag ctg cac agc cac gtc gcc aac atc ggt gac gtg cgc				1152
Asn Ala Leu Lys Leu His Ser His Val Ala Asn Ile Gly Asp Val Arg				
	370	375	380	
tcg ctg gtg atc cac ccg gca tcg acc act cat gcc cag ctg agc ccg				1200
Ser Leu Val Ile His Pro Ala Ser Thr Thr His Ala Gln Leu Ser Pro				
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gcc gag cag ctg gcg acc ggg gtc agc ccg ggc ctg gtg cgt ttg gct				1248
Ala Glu Gln Leu Ala Thr Gly Val Ser Pro Gly Leu Val Arg Leu Ala				
	405	410	415	
gtg ggc atc gaa ggt atc gac gat atc ctg gcc gac ctg gag ctt ggc				1296
Val Gly Ile Glu Gly Ile Asp Asp Ile Leu Ala Asp Leu Glu Leu Gly				
	420	425	430	
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ttc tga				1350
Phe				

<211> 449

<212> PRT

<213> Mycobacterium tuberculosis

<400> 4

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Thr Asn Ala Arg Ala Leu Pro Ile Tyr Ala Thr Thr Ser Tyr Thr Phe
35 40 45

Asp Asp Thr Ala His Ala Ala Ala Leu Phe Gly Leu Glu Ile Pro Gly
50 55 60

Asn Ile Tyr Thr Arg Ile Gly Asn Pro Thr Thr Asp Val Val Glu Gln
65 70 75 80

Arg Ile Ala Ala Leu Glu Gly Gly Val Ala Ala Leu Phe Leu Ser Ser
85 90 95

Gly Gln Ala Ala Glu Thr Phe Ala Ile Leu Asn Leu Ala Gly Ala Gly
100 105 110

Asp His Ile Val Ser Ser Pro Arg Leu Tyr Gly Gly Thr Tyr Asn Leu
115 120 125

Phe His Tyr Ser Leu Ala Lys Leu Gly Ile Glu Val Ser Phe Val Asp
130 135 140

Asp Pro Asp Asp Leu Asp Thr Trp Gln Ala Ala Val Arg Pro Asn Thr
145 150 155 160

Lys Ala Phe Phe Ala Glu Thr Ile Ser Asn Pro Gln Ile Asp Leu Leu
165 170 175

Asp Thr Pro Ala Val Ser Glu Val Ala His Arg Asn Gly Val Pro Leu
180 185 190

Ile Val Asp Asn Thr Ile Ala Thr Pro Tyr Leu Ile Gln Pro Leu Ala

195

200

205

Gln Gly Ala Asp Ile Val Val His Ser Ala Thr Lys Tyr Leu Gly Gly
 210 215 220

His Gly Ala Ala Ile Ala Gly Val Ile Val Asp Gly Gly Asn Phe Asp
 225 230 235 240

Trp Thr Gln Gly Arg Phe Pro Gly Phe Thr Thr Pro Asp Pro Ser Tyr
 245 250 255

His Gly Val Val Phe Ala Glu Leu Gly Pro Pro Ala Phe Ala Leu Lys
 260 265 270

Ala Arg Val Gln Leu Leu Arg Asp Tyr Gly Ser Ala Ala Ser Pro Phe
 275 280 285

Asn Ala Phe Leu Val Ala Gln Gly Leu Glu Thr Leu Ser Leu Arg Ile
 290 295 300

Glu Arg His Val Ala Asn Ala Gln Arg Val Ala Glu Phe Leu Ala Ala
 305 310 315 320

Arg Asp Asp Val Leu Ser Val Asn Tyr Ala Gly Leu Pro Ser Ser Pro
 325 330 335

Trp His Glu Arg Ala Lys Arg Leu Ala Pro Lys Gly Thr Gly Ala Val
 340 345 350

Leu Ser Phe Glu Leu Ala Gly Gly Ile Glu Ala Gly Lys Ala Phe Val
 355 360 365

Asn Ala Leu Lys Leu His Ser His Val Ala Asn Ile Gly Asp Val Arg
 370 375 380

Ser Leu Val Ile His Pro Ala Ser Thr Thr His Ala Gln Leu Ser Pro
 385 390 395 400

Ala Glu Gln Leu Ala Thr Gly Val Ser Pro Gly Leu Val Arg Leu Ala
 405 410 415

Val Gly Ile Glu Gly Ile Asp Asp Ile Leu Ala Asp Leu Glu Leu Gly
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Phe Ala Ala Ala Arg Arg Phe Ser Ala Asp Pro Gln Ser Val Ala Ala

435

440

445

Phe

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<211> 1284

<212> DNA

<213> Clostridium acetobutylicum

<220>

<221> CDS

<222> (1) .. (1284)

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Gly Gln Val Ala Asp Pro Thr Thr Gly Ser Arg Ala Val Pro Ile Tyr	
20 25 30	
caa aca aca tca tat gta ttt aaa aat gct gat cat gca gca aat tta	144
Gln Thr Thr Ser Tyr Val Phe Lys Asn Ala Asp His Ala Ala Asn Leu	
35 40 45	
ttt caa ttg aaa gaa cct gga aat gta tat aca agg ata atg aat cca	192
Phe Gln Leu Lys Glu Pro Gly Asn Val Tyr Thr Arg Ile Met Asn Pro	
50 55 60	
aca act gat gta ttt gaa caa aga gta gca gct ctt gag ggc gga gtt	240
Thr Thr Asp Val Phe Glu Gln Arg Val Ala Ala Leu Glu Gly Gly Val	
65 70 75 80	
gct gga ctt gca aca gca tca gga ctt gca gca att acc tat gct att	288
Ala Gly Leu Ala Thr Ala Ser Gly Leu Ala Ala Ile Thr Tyr Ala Ile	
85 90 95	
tta aat gtg gca agt gct ggg gat gaa att gtt gca gca agt acc tta	336
Leu Asn Val Ala Ser Ala Gly Asp Glu Ile Val Ala Ala Ser Thr Leu	
100 105 110	
tat ggt gga aca tat gaa tta ttt ggg gtt act ctt aag aag ctt gga	384
Tyr Gly Gly Thr Tyr Glu Leu Phe Gly Val Thr Leu Lys Lys Leu Gly	
115 120 125	
ata aag gtt gtt ttt gta gat cca gat aat cct gaa aat ata aga aaa	432
Ile Lys Val Val Phe Val Asp Pro Asp Asn Pro Glu Asn Ile Arg Lys	
130 135 140	

gca ata aat gat agg aca aaa gct gta tat ggg gaa act att gga aat	480
Ala Ile Asn Asp Arg Thr Lys Ala Val Tyr Gly Glu Thr Ile Gly Asn	
145 150 155 160	
cca aga ata aat gtt ttg gat ata gag gca gta gct aaa att gcc cat	528
Pro Arg Ile Asn Val Leu Asp Ile Glu Ala Val Ala Lys Ile Ala His	
165 170 175	
gaa aat aaa ata cca ctt ata atc gat aat aca ttt ggt aca ccg tat	576
Glu Asn Lys Ile Pro Leu Ile Ile Asp Asn Thr Phe Gly Thr Pro Tyr	
180 185 190	
ctt ata aga cct ata gaa ttt gga gca gat ata gtt gta cat tca gca	624
Leu Ile Arg Pro Ile Glu Phe Gly Ala Asp Ile Val Val His Ser Ala	
195 200 205	
aca aag ttt ata gga gga cat gga act act ata ggt gga att ata gtt	672
Thr Lys Phe Ile Gly Gly His Gly Thr Thr Ile Gly Gly Ile Ile Val	
210 215 220	
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Asp Gly Gly Lys Phe Asp Trp Arg Ala Ser Gly Lys Phe Pro Asp Phe	
225 230 235 240	
aca aca ccg gat aag agc tat aat gga ctt ata tat gct gat cta ggt	768
Thr Thr Pro Asp Lys Ser Tyr Asn Gly Leu Ile Tyr Ala Asp Leu Gly	
245 250 255	
gca cct gct ttt gct tta aaa gca aga gtt caa ctt tta aga aat aca	816
Ala Pro Ala Phe Ala Leu Lys Ala Arg Val Gln Leu Leu Arg Asn Thr	
260 265 270	
ggt gca acg ctt agt cca caa agt gct ttt tat ttc cta caa ggg ttg	864
Gly Ala Thr Leu Ser Pro Gln Ser Ala Phe Tyr Phe Leu Gln Gly Leu	
275 280 285	
gaa tca ctt tca ctt agg gtt caa aaa cat gtt gat aat aca aga aag	912
Glu Ser Leu Ser Leu Arg Val Gln Lys His Val Asp Asn Thr Arg Lys	
290 295 300	
gta gtt gaa ttc ttg aag aac cat cca aaa gtt tca tgg ata aat tat	960
Val Val Glu Phe Leu Lys Asn His Pro Lys Val Ser Trp Ile Asn Tyr	
305 310 315 320	
cct gaa ctt gag gaa agt cct tat aaa gag tta gca aat aaa tat ctt	1008
Pro Glu Leu Glu Glu Ser Pro Tyr Lys Glu Leu Ala Asn Lys Tyr Leu	
325 330 335	
cca aag ggt gca ggc tca ata ttt aca ttt gga ata aag gga gga ctt	1056
Pro Lys Gly Ala Gly Ser Ile Phe Thr Phe Gly Ile Lys Gly Gly Leu	
340 345 350	
gaa gct ggt aaa aga ttt ata aat agt gtt aaa cta ttc tct ctt ttg	1104
Glu Ala Gly Lys Arg Phe Ile Asn Ser Val Lys Leu Phe Ser Leu Leu	
355 360 365	
gca aat gtt gca gat gca aaa tca ctt gtt ata cat cct tca agt aca	1152
Ala Asn Val Ala Asp Ala Lys Ser Leu Val Ile His Pro Ser Ser Thr	
370 375 380	

act cat gct gaa ctt aat gaa gaa gaa caa aaa gca gct ggt gtt act 1200
 Thr His Ala Glu Leu Asn Glu Glu Glu Gln Lys Ala Ala Gly Val Thr
 385 390 395 400

cca gat atg ata aga ctt tca ata gga gta gag gat gca gag gat tta 1248
 Pro Asp Met Ile Arg Leu Ser Ile Gly Val Glu Asp Ala Glu Asp Leu
 405 410 415

ata tgg gac tta aat caa gct ctc gaa caa gct taa 1284
 Ile Trp Asp Leu Asn Gln Ala Leu Glu Gln Ala
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<210> 6

<211> 427

<212> PRT

<213> Clostridium acetobutylicum

<400> 6

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Gln Thr Thr Ser Tyr Val Phe Lys Asn Ala Asp His Ala Ala Asn Leu
 35 40 45

Phe Gln Leu Lys Glu Pro Gly Asn Val Tyr Thr Arg Ile Met Asn Pro
 50 55 60

Thr Thr Asp Val Phe Glu Gln Arg Val Ala Ala Leu Glu Gly Gly Val
 65 70 75 80

Ala Gly Leu Ala Thr Ala Ser Gly Leu Ala Ala Ile Thr Tyr Ala Ile
 85 90 95

Leu Asn Val Ala Ser Ala Gly Asp Glu Ile Val Ala Ala Ser Thr Leu
 100 105 110

Tyr Gly Gly Thr Tyr Glu Leu Phe Gly Val Thr Leu Lys Lys Leu Gly
 115 120 125

Ile Lys Val Val Phe Val Asp Pro Asp Asn Pro Glu Asn Ile Arg Lys
 130 135 140

Ala Ile Asn Asp Arg Thr Lys Ala Val Tyr Gly Glu Thr Ile Gly Asn
145 150 155 160

Pro Arg Ile Asn Val Leu Asp Ile Glu Ala Val Ala Lys Ile Ala His
165 170 175

Glu Asn Lys Ile Pro Leu Ile Ile Asp Asn Thr Phe Gly Thr Pro Tyr
180 185 190

Leu Ile Arg Pro Ile Glu Phe Gly Ala Asp Ile Val Val His Ser Ala
195 200 205

Thr Lys Phe Ile Gly Gly His Gly Thr Thr Ile Gly Gly Ile Ile Val
210 215 220

Asp Gly Gly Lys Phe Asp Trp Arg Ala Ser Gly Lys Phe Pro Asp Phe
225 230 235 240

Thr Thr Pro Asp Lys Ser Tyr Asn Gly Leu Ile Tyr Ala Asp Leu Gly
245 250 255

Ala Pro Ala Phe Ala Leu Lys Ala Arg Val Gln Leu Leu Arg Asn Thr
260 265 270

Gly Ala Thr Leu Ser Pro Gln Ser Ala Phe Tyr Phe Leu Gln Gly Leu
275 280 285

Glu Ser Leu Ser Leu Arg Val Gln Lys His Val Asp Asn Thr Arg Lys
290 295 300

Val Val Glu Phe Leu Lys Asn His Pro Lys Val Ser Trp Ile Asn Tyr
305 310 315 320

Pro Glu Leu Glu Glu Ser Pro Tyr Lys Glu Leu Ala Asn Lys Tyr Leu
325 330 335

Pro Lys Gly Ala Gly Ser Ile Phe Thr Phe Gly Ile Lys Gly Gly Leu
340 345 350

Glu Ala Gly Lys Arg Phe Ile Asn Ser Val Lys Leu Phe Ser Leu Leu
355 360 365

Ala Asn Val Ala Asp Ala Lys Ser Leu Val Ile His Pro Ser Ser Thr

370

375

380

Thr His Ala Glu Leu Asn Glu Glu Glu Gln Lys Ala Ala Gly Val Thr
 385 390 395 400

Pro Asp Met Ile Arg Leu Ser Ile Gly Val Glu Asp Ala Glu Asp Leu
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Ile Trp Asp Leu Asn Gln Ala Leu Glu Gln Ala
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<210> 7

<211> 1293

<212> DNA

<213> Bacillus halodurans

<220>

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 Gly Gln Glu Ile Asp Pro Thr Thr Leu Ser Arg Ala Val Pro Leu Tyr
 20 25 30

caa acg acg tcc tac gga ttt aaa gat aca gac cat gcg gcg aat tta 144
 Gln Thr Thr Ser Tyr Gly Phe Lys Asp Thr Asp His Ala Ala Asn Leu
 35 40 45

ttt tca cta agt gaa ttt ggc aat atc tat acc cga ttg atg aac cca 192
 Phe Ser Leu Ser Glu Phe Gly Asn Ile Tyr Thr Arg Leu Met Asn Pro
 50 55 60

acg aca gat gtg ttt gaa aaa cgt gtg gct gcg tta gaa gga gga gcg 240
 Thr Thr Asp Val Phe Glu Lys Arg Val Ala Ala Leu Glu Gly Gly Ala
 65 70 75 80

gca gct tta gcg acg gcc tca ggg cag gcg gcc att acg tat tgg att 288
 Ala Ala Leu Ala Thr Ala Ser Gly Gln Ala Ala Ile Thr Tyr Ser Ile
 85 90 95

tta aat att gcg gag gct gga gat gaa atc gtg tcc gct agt agc ctt 336
 Leu Asn Ile Ala Glu Ala Gly Asp Glu Ile Val Ser Ala Ser Ser Leu

100	105	110	
tac ggc gga acg tat aat tta ttt tcg att acg ttg cca aag cta ggg Tyr Gly Gly Thr Tyr Asn Leu Phe Ser Ile Thr Leu Pro Lys Leu Gly 115 120 125			384
gta aac gtc cgt ttc gtt gat cca tcg gac cca gaa aac ttc aaa gca Val Asn Val Arg Phe Val Asp Pro Ser Asp Pro Glu Asn Phe Lys Ala 130 135 140			432
gcg att act gaa aag acg aaa gcc att ttc gct gag tcg att gga aac Ala Ile Thr Glu Lys Thr Lys Ala Ile Phe Ala Glu Ser Ile Gly Asn 145 150 155 160			480
cct aag gga gac gtg tta gat att gaa gcg gtg gcg aaa gtt gca cac Pro Lys Gly Asp Val Leu Asp Ile Glu Ala Val Ala Lys Val Ala His 165 170 175			528
gat cat cac ctt ccc ctc att gtc gat aac acg ttt cca agc cca tat Asp His His Leu Pro Leu Ile Val Asp Asn Thr Phe Pro Ser Pro Tyr 180 185 190			576
ttg ctt caa ccg ata aag cac ggc gca gac att gtt gtg cat tca gca Leu Leu Gln Pro Ile Lys His Gly Ala Asp Ile Val Val His Ser Ala 195 200 205			624
aca aaa ttt atc ggt ggt cat ggg acg tcg ata gga ggg atc att gtc Thr Lys Phe Ile Gly Gly His Gly Thr Ser Ile Gly Gly Ile Ile Val 210 215 220			672
gat gga ggg acg ttt gat tgg gcg aaa acg gat cga tat cca ggg cta Asp Gly Gly Thr Phe Asp Trp Ala Lys Thr Asp Arg Tyr Pro Gly Leu 225 230 235 240			720
aca aca cct gat ccg agt tac cac ggt gtt gta tat aca gat gcg gtc Thr Thr Pro Asp Pro Ser Tyr His Gly Val Val Tyr Thr Asp Ala Val 245 250 255			768
ggt cca att gct tat att att aaa gcg cgt gtt cag cta ttg cgt gac Gly Pro Ile Ala Tyr Ile Ile Lys Ala Arg Val Gln Leu Leu Arg Asp 260 265 270			816
atg ggg gca gcc ata tcg cca ttt aac tcg ttt tta ctg ttg caa ggg Met Gly Ala Ala Ile Ser Pro Phe Asn Ser Phe Leu Leu Leu Gln Gly 275 280 285			864
ttg gaa acg ttg cat tta cgg atg gag aga cat agt gaa aat gcc tac Leu Glu Thr Leu His Leu Arg Met Glu Arg His Ser Glu Asn Ala Tyr 290 295 300			912
aaa gta gca gag ttc ctt gag caa cat caa gcg gtc gaa tcg gtg agc Lys Val Ala Glu Phe Leu Glu Gln His Gln Ala Val Glu Ser Val Ser 305 310 315 320			960
tac tct gga ctg cca tcc cat cca tcc tac cca tta gcg aaa aaa tac Tyr Ser Gly Leu Pro Ser His Pro Ser Tyr Pro Leu Ala Lys Lys Tyr 325 330 335			1008
tta cct aaa ggc caa ggg gct atc tta acg ttc gag gta aag ggc ggc Leu Pro Lys Gly Gln Gly Ala Ile Leu Thr Phe Glu Val Lys Gly Gly 340 345 350 355			1056

340

345

350

gtt gaa gca gga aag aaa ctc att cat tcg gtc cag cta ttc tcc cac 1104
 Val Glu Ala Gly Lys Lys Leu Ile His Ser Val Gln Leu Phe Ser His
 355 360 365

ctt gcc aac gta ggt gat tca aaa tcg ttg atc atc cat cct gca agc 1152
 Leu Ala Asn Val Gly Asp Ser Lys Ser Leu Ile Ile His Pro Ala Ser
 370 375 380

acg acc cac caa cag ctc tcg gaa gca gaa cag cga gac gca gga gtg 1200
 Thr Thr His Gln Gln Leu Ser Glu Ala Glu Gln Arg Asp Ala Gly Val
 385 390 395 400

aca cct ggg atg atc aga ctt tcg gta gga acc gaa tcg att cat gat 1248
 Thr Pro Gly Met Ile Arg Leu Ser Val Gly Thr Glu Ser Ile His Asp
 405 410 415

att atc acc gat ctc aaa cag gcg att gag gcg agt caa gcg taa 1293
 Ile Ile Thr Asp Leu Lys Gln Ala Ile Glu Ala Ser Gln Ala
 420 425 430

<210> 8

<211> 430

<212> PRT

<213> Bacillus halodurans

<400> 8

Met Asn His Glu Asn Gln Trp Gln Leu Glu Thr Lys Ala Val His Ser
 1 5 10 15

Gly Gln Glu Ile Asp Pro Thr Thr Leu Ser Arg Ala Val Pro Leu Tyr
 20 25 30

Gln Thr Thr Ser Tyr Gly Phe Lys Asp Thr Asp His Ala Ala Asn Leu
 35 40 45

Phe Ser Leu Ser Glu Phe Gly Asn Ile Tyr Thr Arg Leu Met Asn Pro
 50 55 60

Thr Thr Asp Val Phe Glu Lys Arg Val Ala Ala Leu Glu Gly Gly Ala
 65 70 75 80

Ala Ala Leu Ala Thr Ala Ser Gly Gln Ala Ala Ile Thr Tyr Ser Ile
 85 90 95

Leu Asn Ile Ala Glu Ala Gly Asp Glu Ile Val Ser Ala Ser Ser Leu

100

105

110

Tyr Gly Gly Thr Tyr Asn Leu Phe Ser Ile Thr Leu Pro Lys Leu Gly
 115 120 125

Val Asn Val Arg Phe Val Asp Pro Ser Asp Pro Glu Asn Phe Lys Ala
 130 135 140

Ala Ile Thr Glu Lys Thr Lys Ala Ile Phe Ala Glu Ser Ile Gly Asn
 145 150 155 160

Pro Lys Gly Asp Val Leu Asp Ile Glu Ala Val Ala Lys Val Ala His
 165 170 175

Asp His His Leu Pro Leu Ile Val Asp Asn Thr Phe Pro Ser Pro Tyr
 180 185 190

Leu Leu Gln Pro Ile Lys His Gly Ala Asp Ile Val Val His Ser Ala
 195 200 205

Thr Lys Phe Ile Gly Gly His Gly Thr Ser Ile Gly Gly Ile Ile Val
 210 215 220

Asp Gly Gly Thr Phe Asp Trp Ala Lys Thr Asp Arg Tyr Pro Gly Leu
 225 230 235 240

Thr Thr Pro Asp Pro Ser Tyr His Gly Val Val Tyr Thr Asp Ala Val
 245 250 255

Gly Pro Ile Ala Tyr Ile Ile Lys Ala Arg Val Gln Leu Leu Arg Asp
 260 265 270

Met Gly Ala Ala Ile Ser Pro Phe Asn Ser Phe Leu Leu Leu Gln Gly
 275 280 285

Leu Glu Thr Leu His Leu Arg Met Glu Arg His Ser Glu Asn Ala Tyr
 290 295 300

Lys Val Ala Glu Phe Leu Glu Gln His Gln Ala Val Glu Ser Val Ser
 305 310 315 320

Tyr Ser Gly Leu Pro Ser His Pro Ser Tyr Pro Leu Ala Lys Lys Tyr
 325 330 335

Leu Pro Lys Gly Gln Gly Ala Ile Leu Thr Phe Glu Val Lys Gly Gly

340

345

350

Val Glu Ala Gly Lys Lys Leu Ile His Ser Val Gln Leu Phe Ser His
 355 360 365

Leu Ala Asn Val Gly Asp Ser Lys Ser Leu Ile Ile His Pro Ala Ser
 370 375 380

Thr Thr His Gln Gln Leu Ser Glu Ala Glu Gln Arg Asp Ala Gly Val
 385 390 395 400

Thr Pro Gly Met Ile Arg Leu Ser Val Gly Thr Glu Ser Ile His Asp
 405 410 415

Ile Ile Thr Asp Leu Lys Gln Ala Ile Glu Ala Ser Gln Ala
 420 425 430

<210> 9

<211> 1203

<212> DNA

<213> Bacillus stearothermophilus

<220>

<221> CDS

<222> (1) .. (1203)

<400> 9

atg tcg tat gta ttc cgc gac agc gag cac gcg gcc aat ttg ttt ggt 48
 Met Ser Tyr Val Phe Arg Asp Ser Glu His Ala Ala Asn Leu Phe Gly
 1 5 10 15

ttg aaa gag gaa ggt ttt att tat acg cgc att atg aat cca acg aac 96
 Leu Lys Glu Glu Gly Phe Ile Tyr Thr Arg Ile Met Asn Pro Thr Asn
 20 25 30

gac gtg ttc gaa aag cgg atc gcg gcg ctt gaa ggc ggc att ggg gcg 144
 Asp Val Phe Glu Lys Arg Ile Ala Ala Leu Glu Gly Gly Ile Gly Ala
 35 40 45

ctc gcg ctg tca tcg ggg cag gcg gcg gtg ttt tat tcg atc atc aac 192
 Leu Ala Leu Ser Ser Gly Gln Ala Ala Val Phe Tyr Ser Ile Ile Asn
 50 55 60

atc gcc tcg gcg ggc gat gaa atc gtc tcg tct tcg tcc att tac ggc 240

Ile Ala Ser Ala Gly Asp Glu Ile Val Ser Ser Ser Ser Ile Tyr Gly	
65 70 75 80	
gga acg tac aac ttg ttc gcc cat acg ctg cgc aag ttc ggc att acg	288
Gly Thr Tyr Asn Leu Phe Ala His Thr Leu Arg Lys Phe Gly Ile Thr	
85 90 95	
gtg aag ttt gtc gat ccg tcc gac ccc gaa aac ttt gag cgg gcg atc	336
Val Lys Phe Val Asp Pro Ser Asp Pro Glu Asn Phe Glu Arg Ala Ile	
100 105 110	
acc gac aaa acg aaa gcc ttg ttt gcg gaa acg atc ggc aac ccg aaa	384
Thr Asp Lys Thr Lys Ala Leu Phe Ala Glu Thr Ile Gly Asn Pro Lys	
115 120 125	
aac gat gtg ttg gac att gaa gcg gtg gcc gac atc gcc cat cgc cat	432
Asn Asp Val Leu Asp Ile Glu Ala Val Ala Asp Ile Ala His Arg His	
130 135 140	
gcc att ccg ctc att gtc gac aac acg gtg gcc agt cca tac tta ttg	480
Ala Ile Pro Leu Ile Val Asp Asn Thr Val Ala Ser Pro Tyr Leu Leu	
145 150 155 160	
cgg ccg att gaa ttc ggc gcc gat atc gtc gtc cac tca gcg acg aag	528
Arg Pro Ile Glu Phe Gly Ala Asp Ile Val Val His Ser Ala Thr Lys	
165 170 175	
ttc atc ggc ggg cac ggc aat tcg atc ggc ggt gtg att gtg gac agc	576
Phe Ile Gly Gly His Gly Asn Ser Ile Gly Gly Val Ile Val Asp Ser	
180 185 190	
ggc aag ttt gac tgg aaa ggg agc ggc aag ttt ccg gag ttc acc gag	624
Gly Lys Phe Asp Trp Lys Gly Ser Gly Lys Phe Pro Glu Phe Thr Glu	
195 200 205	
cca gac cca agc tac cac ggt ttg gtg tat gtg gac gcc gtc ggc gaa	672
Pro Asp Pro Ser Tyr His Gly Leu Val Tyr Val Asp Ala Val Gly Glu	
210 215 220	
gcg gcg tac atc acg aaa gcg cgc atc cag ctc ttg cgc gat ttg gga	720
Ala Ala Tyr Ile Thr Lys Ala Arg Ile Gln Leu Leu Arg Asp Leu Gly	
225 230 235 240	
gcg gcg ttg tcg ccg ttt aat gcg ttt ttg ctt ttg caa ggg ttg gag	768
Ala Ala Leu Ser Pro Phe Asn Ala Phe Leu Leu Leu Gln Gly Leu Glu	
245 250 255	
acg ctc cat ttg cgg atg cag cgc cat agc gaa aac gcc ctt gcc gtc	816
Thr Leu His Leu Arg Met Gln Arg His Ser Glu Asn Ala Leu Ala Val	
260 265 270	
gcc aag ttt tta gaa gag gaa gaa gcg gtc gaa tcg gtc aat tac cca	864
Ala Lys Phe Leu Glu Glu Glu Glu Ala Val Glu Ser Val Asn Tyr Pro	
275 280 285	
ggg ctt ccg agc cat ccg tcg cat gaa ctg gcg aaa aaa tat ttg cca	912
Gly Leu Pro Ser His Pro Ser His Glu Leu Ala Lys Lys Tyr Leu Pro	
290 295 300	
aac ggg caa gga gcg atc gtc acg ttt gaa atc aaa ggc ggc gtc gaa	960

Asn Gly Gln Gly Ala Ile Val Thr Phe Glu Ile Lys Gly Gly Val Glu
 305 310 315 320

 gcc gcc aaa aaa ctg atc gac tcg gtc aaa ctg ttc tct cat ttg gcc 1008
 Ala Gly Lys Lys Leu Ile Asp Ser Val Lys Leu Phe Ser His Leu Ala
 325 330 335

 aac atc gcc gat tcg aaa tcg ctc atc atc cac ccg gcc agc aca acg 1056
 Asn Ile Gly Asp Ser Lys Ser Leu Ile Ile His Pro Ala Ser Thr Thr
 340 345 350

 cac gag cag ctg agc cca gat gaa cag ctg tcc gcc gcc gtc acc cca 1104
 His Glu Gln Leu Ser Pro Asp Glu Gln Leu Ser Ala Gly Val Thr Pro
 355 360 365

 gcc ctt gtg cgt ctg tcc gtc gcc aca gaa gcg atc gac gac att ttg 1152
 Gly Leu Val Arg Leu Ser Val Gly Thr Glu Ala Ile Asp Asp Ile Leu
 370 375 380

 gac gac ttg cgc caa gcc att cgc caa agc cag acg gtg ggg gtg aag 1200
 Asp Asp Leu Arg Gln Ala Ile Arg Gln Ser Gln Thr Val Gly Val Lys
 385 390 395 400

 tag 1203

<210> 10

<211> 400

<212> PRT

<213> Bacillus stearothermophilus

<400> 10

Met Ser Tyr Val Phe Arg Asp Ser Glu His Ala Ala Asn Leu Phe Gly
 1 5 10 15

 Leu Lys Glu Glu Gly Phe Ile Tyr Thr Arg Ile Met Asn Pro Thr Asn
 20 25 30

 Asp Val Phe Glu Lys Arg Ile Ala Ala Leu Glu Gly Gly Ile Gly Ala
 35 40 45

 Leu Ala Leu Ser Ser Gly Gln Ala Ala Val Phe Tyr Ser Ile Ile Asn
 50 55 60

 Ile Ala Ser Ala Gly Asp Glu Ile Val Ser Ser Ser Ser Ile Tyr Gly
 65 70 75 80

 Gly Thr Tyr Asn Leu Phe Ala His Thr Leu Arg Lys Phe Gly Ile Thr
 85 90 95

Val Lys Phe Val Asp Pro Ser Asp Pro Glu Asn Phe Glu Arg Ala Ile
 100 105 110

Thr Asp Lys Thr Lys Ala Leu Phe Ala Glu Thr Ile Gly Asn Pro Lys
 115 120 125

Asn Asp Val Leu Asp Ile Glu Ala Val Ala Asp Ile Ala His Arg His
 130 135 140

Ala Ile Pro Leu Ile Val Asp Asn Thr Val Ala Ser Pro Tyr Leu Leu
 145 150 155 160

Arg Pro Ile Glu Phe Gly Ala Asp Ile Val Val His Ser Ala Thr Lys
 165 170 175

Phe Ile Gly Gly His Gly Asn Ser Ile Gly Gly Val Ile Val Asp Ser
 180 185 190

Gly Lys Phe Asp Trp Lys Gly Ser Gly Lys Phe Pro Glu Phe Thr Glu
 195 200 205

Pro Asp Pro Ser Tyr His Gly Leu Val Tyr Val Asp Ala Val Gly Glu
 210 215 220

Ala Ala Tyr Ile Thr Lys Ala Arg Ile Gln Leu Leu Arg Asp Leu Gly
 225 230 235 240

Ala Ala Leu Ser Pro Phe Asn Ala Phe Leu Leu Leu Gln Gly Leu Glu
 245 250 255

Thr Leu His Leu Arg Met Gln Arg His Ser Glu Asn Ala Leu Ala Val
 260 265 270

Ala Lys Phe Leu Glu Glu Glu Glu Ala Val Glu Ser Val Asn Tyr Pro
 275 280 285

Gly Leu Pro Ser His Pro Ser His Glu Leu Ala Lys Lys Tyr Leu Pro
 290 295 300

Asn Gly Gln Gly Ala Ile Val Thr Phe Glu Ile Lys Gly Gly Val Glu
 305 310 315 320

Ala Gly Lys Lys Leu Ile Asp Ser Val Lys Leu Phe Ser His Leu Ala

325

330

335

Asn Ile Gly Asp Ser Lys Ser Leu Ile Ile His Pro Ala Ser Thr Thr
 340 345 350

His Glu Gln Leu Ser Pro Asp Glu Gln Leu Ser Ala Gly Val Thr Pro
 355 360 365

Gly Leu Val Arg Leu Ser Val Gly Thr Glu Ala Ile Asp Asp Ile Leu
 370 375 380

Asp Asp Leu Arg Gln Ala Ile Arg Gln Ser Gln Thr Val Gly Val Lys
 385 390 395 400

<210> 11

<211> 1290

<212> DNA

<213> Chlorobium tepidum

<220>

<221> CDS

<222> (1)..(1290)

<400> 11

atg agt gag gat aac acc ttc cgg ttc gag acc ttg cag gtt cac gcc 48
 Met Ser Glu Asp Asn Thr Phe Arg Phe Glu Thr Leu Gln Val His Ala
 1 5 10 15

ggg cag gag cct gat ccg gtg acc gga tcg cgc gcc gtg ccc att tac 96
 Gly Gln Glu Pro Asp Pro Val Thr Gly Ser Arg Ala Val Pro Ile Tyr
 20 25 30

cag acc acc tcc tac gtg ttc gag aac gcc gag cac ggc gct gac ctg 144
 Gln Thr Thr Ser Tyr Val Phe Glu Asn Ala Glu His Gly Ala Asp Leu
 35 40 45

ttc gcg ctt cgc aag gcg ggc aat atc tac acg cgc ctg atg aac ccg 192
 Phe Ala Leu Arg Lys Ala Gly Asn Ile Tyr Thr Arg Leu Met Asn Pro
 50 55 60

acc acc gac gtg ctc gaa aag cgc atg gcg gcg ctc gaa ggg ggc aag 240
 Thr Thr Asp Val Leu Glu Lys Arg Met Ala Ala Leu Glu Gly Gly Lys
 65 70 75 80

gcg gcc ctc ggc gtg gcg agc ggc cac tcg gcg cag ttc atc gct att 288

Ala Ala Leu Gly Val Ala Ser Gly His Ser Ala Gln Phe Ile Ala Ile	
85 90 95	
gcc acc atc tgc cag gct gga gac aac att gtg tca tcg agc tat ctc	336
Ala Thr Ile Cys Gln Ala Gly Asp Asn Ile Val Ser Ser Ser Tyr Leu	
100 105 110	
tac ggc ggc acc tac aac cag ttc aag gtc gcc ttc aag cgc ctc ggc	384
Tyr Gly Gly Thr Tyr Asn Gln Phe Lys Val Ala Phe Lys Arg Leu Gly	
115 120 125	
atc gag gtg agg ttc gtg gat ggc aac gat cag gag gcg ttc cgc aag	432
Ile Glu Val Arg Phe Val Asp Gly Asn Asp Gln Glu Ala Phe Arg Lys	
130 135 140	
gct atc gac gag aac acg aaa gcg ctc tac atg gag tcc agc ggc aat	480
Ala Ile Asp Glu Asn Thr Lys Ala Leu Tyr Met Glu Ser Ser Gly Asn	
145 150 155 160	
ccg gcg ttc cat gtg ccc gat ttc gac gct atc gcg aag att gcc cgt	528
Pro Ala Phe His Val Pro Asp Phe Asp Ala Ile Ala Lys Ile Ala Arg	
165 170 175	
gag aac ggc att ccg ctg atc gtc gat aac acc ttt ggc tgc gcg ggc	576
Glu Asn Gly Ile Pro Leu Ile Val Asp Asn Thr Phe Gly Cys Ala Gly	
180 185 190	
tat ctc tgc cgt ccc att gat cac ggc gcg tcg atc gtg gtc gag tcg	624
Tyr Leu Cys Arg Pro Ile Asp His Gly Ala Ser Ile Val Val Glu Ser	
195 200 205	
gcc acc aag tgg atc ggc ggg cac ggc acc tcg atg ggc ggc atc atc	672
Ala Thr Lys Trp Ile Gly Gly His Gly Thr Ser Met Gly Gly Ile Ile	
210 215 220	
gtc gat gcc gga acg ttc gac tgg ggc aac ggc aag ttt ccg ctc ttt	720
Val Asp Ala Gly Thr Phe Asp Trp Gly Asn Gly Lys Phe Pro Leu Phe	
225 230 235 240	
acc gag cca tcg gaa ggc tat cac ggc ctg aaa ttc tac gaa gcg gtc	768
Thr Glu Pro Ser Glu Gly Tyr His Gly Leu Lys Phe Tyr Glu Ala Val	
245 250 255	
ggc gag ctg gcc ttt atc atc cgg gcg cgg gtc gag gga ctg cgg gat	816
Gly Glu Leu Ala Phe Ile Ile Arg Ala Arg Val Glu Gly Leu Arg Asp	
260 265 270	
ttc ggc ccg gcg atc agc ccg ttc aac tcc ttc atg ctg ttg cag gga	864
Phe Gly Pro Ala Ile Ser Pro Phe Asn Ser Phe Met Leu Leu Gln Gly	
275 280 285	
ctt gaa acg ctc tcg ctt cgc gtg cag cgc cac ctc gac aac acg ctt	912
Leu Glu Thr Leu Ser Leu Arg Val Gln Arg His Leu Asp Asn Thr Leu	
290 295 300	
gaa ctg gcc cgc tgg ctc gaa agg cac gat gcg gtt gcg tgg gtg aac	960
Glu Leu Ala Arg Trp Leu Glu Arg His Asp Ala Val Ala Trp Val Asn	
305 310 315 320	
tat cca ggc ctc gaa agc cat ccg aca cac gcc ctg gca aaa aaa tat	1008

Tyr Pro Gly Leu Glu Ser His Pro Thr His Ala Leu Ala Lys Lys Tyr
 325 330 335
 ctc acg cat ggc ttc ggc tgc gtg ctg act ttc ggc gtg aag ggt ggt 1056
 Leu Thr His Gly Phe Gly Cys Val Leu Thr Phe Gly Val Lys Gly Gly
 340 345 350
 tat gaa aac gcg gtg aag ttc atc gac agc gtg aag ctg gcg agc cac 1104
 Tyr Glu Asn Ala Val Lys Phe Ile Asp Ser Val Lys Leu Ala Ser His
 355 360 365
 ctg gcc aac gtg ggt gat gca aaa acg ctc gtc att cat ccg gca tcg 1152
 Leu Ala Asn Val Gly Asp Ala Lys Thr Leu Val Ile His Pro Ala Ser
 370 375 380
 acg acg cac cag cag ctc agc gcc gag gaa cag gta tcg gcg ggc gtc 1200
 Thr Thr His Gln Gln Leu Ser Ala Glu Glu Gln Val Ser Ala Gly Val
 385 390 395 400
 acc gcc gat atg gtg cgc gtg tcg gtt ggt atc gag cat atc gat gac 1248
 Thr Ala Asp Met Val Arg Val Ser Val Gly Ile Glu His Ile Asp Asp
 405 410 415
 atc aag gct gat ttc agc cag gct ttc gag aat tta gca tga 1290
 Ile Lys Ala Asp Phe Ser Gln Ala Phe Glu Asn Leu Ala
 420 425

 <210> 12
 <211> 429
 <212> PRT
 <213> Chlorobium tepidum

 <400> 12
 Met Ser Glu Asp Asn Thr Phe Arg Phe Glu Thr Leu Gln Val His Ala
 1 5 10 15
 Gly Gln Glu Pro Asp Pro Val Thr Gly Ser Arg Ala Val Pro Ile Tyr
 20 25 30
 Gln Thr Thr Ser Tyr Val Phe Glu Asn Ala Glu His Gly Ala Asp Leu
 35 40 45
 Phe Ala Leu Arg Lys Ala Gly Asn Ile Tyr Thr Arg Leu Met Asn Pro
 50 55 60
 Thr Thr Asp Val Leu Glu Lys Arg Met Ala Ala Leu Glu Gly Gly Lys
 65 70 75 80

Ala Ala Leu Gly Val Ala Ser Gly His Ser Ala Gln Phe Ile Ala Ile
85 90 95

Ala Thr Ile Cys Gln Ala Gly Asp Asn Ile Val Ser Ser Ser Tyr Leu
100 105 110

Tyr Gly Gly Thr Tyr Asn Gln Phe Lys Val Ala Phe Lys Arg Leu Gly
115 120 125

Ile Glu Val Arg Phe Val Asp Gly Asn Asp Gln Glu Ala Phe Arg Lys
130 135 140

Ala Ile Asp Glu Asn Thr Lys Ala Leu Tyr Met Glu Ser Ser Gly Asn
145 150 155 160

Pro Ala Phe His Val Pro Asp Phe Asp Ala Ile Ala Lys Ile Ala Arg
165 170 175

Glu Asn Gly Ile Pro Leu Ile Val Asp Asn Thr Phe Gly Cys Ala Gly
180 185 190

Tyr Leu Cys Arg Pro Ile Asp His Gly Ala Ser Ile Val Val Glu Ser
195 200 205

Ala Thr Lys Trp Ile Gly Gly His Gly Thr Ser Met Gly Gly Ile Ile
210 215 220

Val Asp Ala Gly Thr Phe Asp Trp Gly Asn Gly Lys Phe Pro Leu Phe
225 230 235 240

Thr Glu Pro Ser Glu Gly Tyr His Gly Leu Lys Phe Tyr Glu Ala Val
245 250 255

Gly Glu Leu Ala Phe Ile Ile Arg Ala Arg Val Glu Gly Leu Arg Asp
260 265 270

Phe Gly Pro Ala Ile Ser Pro Phe Asn Ser Phe Met Leu Leu Gln Gly
275 280 285

Leu Glu Thr Leu Ser Leu Arg Val Gln Arg His Leu Asp Asn Thr Leu
290 295 300

Glu Leu Ala Arg Trp Leu Glu Arg His Asp Ala Val Ala Trp Val Asn
305 310 315 320

Tyr Pro Gly Leu Glu Ser His Pro Thr His Ala Leu Ala Lys Lys Tyr
 325 330 335

Leu Thr His Gly Phe Gly Cys Val Leu Thr Phe Gly Val Lys Gly Gly
 340 345 350

Tyr Glu Asn Ala Val Lys Phe Ile Asp Ser Val Lys Leu Ala Ser His
 355 360 365

Leu Ala Asn Val Gly Asp Ala Lys Thr Leu Val Ile His Pro Ala Ser
 370 375 380

Thr Thr His Gln Gln Leu Ser Ala Glu Glu Gln Val Ser Ala Gly Val
 385 390 395 400

Thr Ala Asp Met Val Arg Val Ser Val Gly Ile Glu His Ile Asp Asp
 405 410 415

Ile Lys Ala Asp Phe Ser Gln Ala Phe Glu Asn Leu Ala
 420 425

<210> 13

<211> 1281

<212> DNA

<213> Lactococcus lactis

<220>

<221> CDS

<222> (1)..(1281)

<400> 13

atg act aat cac aat tat aaa ttc gac act ttg caa gtc cat gca gga 48
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 1 5 10 15

caa gtc cct gat cct gtc acg ggt tca cgc gcc gtt ccg ctc tat caa 96
 Gln Val Pro Asp Pro Val Thr Gly Ser Arg Ala Val Pro Leu Tyr Gln
 20 25 30

aca act tct ttc gtt ttt aac aat tca gac cat gcc gaa gct cgt ttt 144
 Thr Thr Ser Phe Val Phe Asn Asn Ser Asp His Ala Glu Ala Arg Phe
 35 40 45

gct tta caa gat cct gga gct att tat tca cgt tta gga aat cca acc Ala Leu Gln Asp Pro Gly Ala Ile Tyr Ser Arg Leu Gly Asn Pro Thr 50 55 60	192
aac gat gtt ttt gaa gca cgc atc gca gct ctt gaa ggt gga agt gca Asn Asp Val Phe Glu Ala Arg Ile Ala Ala Leu Glu Gly Gly Ser Ala 65 70 75 80	240
gcc ctt ggt gtt ggt tct ggc tca gcc gct att acc tat gcc atc ttg Ala Leu Gly Val Gly Ser Gly Ser Ala Ala Ile Thr Tyr Ala Ile Leu 85 90 95	288
aat atc gct aca gtc ggt gat aat att gtt tcc gca agt acc ctt tat Asn Ile Ala Thr Val Gly Asp Asn Ile Val Ser Ala Ser Thr Leu Tyr 100 105 110	336
ggt gga acc tat cac ctt ttt tct ggg act tta cca aaa tat gga att Gly Gly Thr Tyr His Leu Phe Ser Gly Thr Leu Pro Lys Tyr Gly Ile 115 120 125	384
aca act aaa ttt gtc aat cca gat gac ccg aag aat ttt gaa gag gcg Thr Thr Lys Phe Val Asn Pro Asp Asp Pro Lys Asn Phe Glu Glu Ala 130 135 140	432
att gat gaa aaa acc aaa gct att tat tat gaa act ttg ggc aat ccg Ile Asp Glu Lys Thr Lys Ala Ile Tyr Tyr Glu Thr Leu Gly Asn Pro 145 150 155 160	480
gga aat aat gtg att gat tat gat gcc att ggt caa att gct aaa aaa Gly Asn Asn Val Ile Asp Tyr Asp Ala Ile Gly Gln Ile Ala Lys Lys 165 170 175	528
cat gga att ccc gtt att gtt gat gca acg ttt act acc cct gtg acc His Gly Ile Pro Val Ile Val Asp Ala Thr Phe Thr Thr Pro Val Thr 180 185 190	576
ttt aaa cca ttt gaa cat ggt gct aat gta att gtt cat tca gca acg Phe Lys Pro Phe Glu His Gly Ala Asn Val Ile Val His Ser Ala Thr 195 200 205	624
aaa ttc att ggc ggt cat ggt act tct att ggt gga gtc atc gtt gat Lys Phe Ile Gly Gly His Gly Thr Ser Ile Gly Gly Val Ile Val Asp 210 215 220	672
ggc gga aac ttt gat tgg gca aat ggt aat ttt cct gat ttt aca caa Gly Gly Asn Phe Asp Trp Ala Asn Gly Asn Phe Pro Asp Phe Thr Gln 225 230 235 240	720
gct gat gaa agc tac aat ggg att aaa ttt gcc gaa ttg ggt gaa att Ala Asp Glu Ser Tyr Asn Gly Ile Lys Phe Ala Glu Leu Gly Glu Ile 245 250 255	768
gct ttt gtg act cgg gtt aga gct att tta tta cgt gat acg ggt gcg Ala Phe Val Thr Arg Val Arg Ala Ile Leu Leu Arg Asp Thr Gly Ala 260 265 270	816
gct tta tca cct ttt cat tct tgg ctt ttc tta cag ggg cta gaa aca	864

Ala Leu Ser Pro Phe His Ser Trp Leu Phe Leu Gln Gly Leu Glu Thr
 275 280 285

ctc tca ctc cgg gta gaa cgt cac atc tcc aat act aaa aag att gta 912
 Leu Ser Leu Arg Val Glu Arg His Ile Ser Asn Thr Lys Lys Ile Val
 290 295 300

gaa ttt tta gac aat cat cct aag gtg gaa ctt gtt aac cat cct ctg 960
 Glu Phe Leu Asp Asn His Pro Lys Val Glu Leu Val Asn His Pro Leu
 305 310 315 320

ctt gaa agt aat tcc tat cat gcg ctc tat cag aaa tat tat cca aaa 1008
 Leu Glu Ser Asn Ser Tyr His Ala Leu Tyr Gln Lys Tyr Tyr Pro Lys
 325 330 335

gat gct gga tct atc ttt acc ttt gaa ctc aaa gac aaa gat gag aaa 1056
 Asp Ala Gly Ser Ile Phe Thr Phe Glu Leu Lys Asp Lys Asp Glu Lys
 340 345 350

aaa gcg cgt gat ttg att gat cat ctt gaa att ttc tca ctt cta gcc 1104
 Lys Ala Arg Asp Leu Ile Asp His Leu Glu Ile Phe Ser Leu Leu Ala
 355 360 365

aac gtt gga gat acc aaa tca ttg gcc att cat cct gct tcg acc act 1152
 Asn Val Gly Asp Thr Lys Ser Leu Ala Ile His Pro Ala Ser Thr Thr
 370 375 380

cac cag cag ctg aat gcc gaa gaa ctt gct agt gca ggg att tcc aaa 1200
 His Gln Gln Leu Asn Ala Glu Glu Leu Ala Ser Ala Gly Ile Ser Lys
 385 390 395 400

gga acc att cga tta tcg gtt ggt att gaa gat gta act gac ttg att 1248
 Gly Thr Ile Arg Leu Ser Val Gly Ile Glu Asp Val Thr Asp Leu Ile
 405 410 415

gct gat tta gag caa gca tta gaa aaa ata taa 1281
 Ala Asp Leu Glu Gln Ala Leu Glu Lys Ile
 420 425

<210> 14

<211> 426

<212> PRT

<213> Lactococcus lactis

<400> 14

Met Thr Asn His Asn Tyr Lys Phe Asp Thr Leu Gln Val His Ala Gly
 1 5 10 15

Gln Val Pro Asp Pro Val Thr Gly Ser Arg Ala Val Pro Leu Tyr Gln
 20 25 30

Thr Thr Ser Phe Val Phe Asn Asn Ser Asp His Ala Glu Ala Arg Phe
35 40 45

Ala Leu Gln Asp Pro Gly Ala Ile Tyr Ser Arg Leu Gly Asn Pro Thr
50 55 60

Asn Asp Val Phe Glu Ala Arg Ile Ala Ala Leu Glu Gly Gly Ser Ala
65 70 75 80

Ala Leu Gly Val Gly Ser Gly Ser Ala Ala Ile Thr Tyr Ala Ile Leu
85 90 95

Asn Ile Ala Thr Val Gly Asp Asn Ile Val Ser Ala Ser Thr Leu Tyr
100 105 110

Gly Gly Thr Tyr His Leu Phe Ser Gly Thr Leu Pro Lys Tyr Gly Ile
115 120 125

Thr Thr Lys Phe Val Asn Pro Asp Asp Pro Lys Asn Phe Glu Glu Ala
130 135 140

Ile Asp Glu Lys Thr Lys Ala Ile Tyr Tyr Glu Thr Leu Gly Asn Pro
145 150 155 160

Gly Asn Asn Val Ile Asp Tyr Asp Ala Ile Gly Gln Ile Ala Lys Lys
165 170 175

His Gly Ile Pro Val Ile Val Asp Ala Thr Phe Thr Thr Pro Val Thr
180 185 190

Phe Lys Pro Phe Glu His Gly Ala Asn Val Ile Val His Ser Ala Thr
195 200 205

Lys Phe Ile Gly Gly His Gly Thr Ser Ile Gly Gly Val Ile Val Asp
210 215 220

Gly Gly Asn Phe Asp Trp Ala Asn Gly Asn Phe Pro Asp Phe Thr Gln
225 230 235 240

Ala Asp Glu Ser Tyr Asn Gly Ile Lys Phe Ala Glu Leu Gly Glu Ile
245 250 255

Ala Phe Val Thr Arg Val Arg Ala Ile Leu Leu Arg Asp Thr Gly Ala
260 265 270

Ala Leu Ser Pro Phe His Ser Trp Leu Phe Leu Gln Gly Leu Glu Thr
 275 280 285

Leu Ser Leu Arg Val Glu Arg His Ile Ser Asn Thr Lys Lys Ile Val
 290 295 300

Glu Phe Leu Asp Asn His Pro Lys Val Glu Leu Val Asn His Pro Leu
 305 310 315 320

Leu Glu Ser Asn Ser Tyr His Ala Leu Tyr Gln Lys Tyr Tyr Pro Lys
 325 330 335

Asp Ala Gly Ser Ile Phe Thr Phe Glu Leu Lys Asp Lys Asp Glu Lys
 340 345 350

Lys Ala Arg Asp Leu Ile Asp His Leu Glu Ile Phe Ser Leu Leu Ala
 355 360 365

Asn Val Gly Asp Thr Lys Ser Leu Ala Ile His Pro Ala Ser Thr Thr
 370 375 380

His Gln Gln Leu Asn Ala Glu Glu Leu Ala Ser Ala Gly Ile Ser Lys
 385 390 395 400

Gly Thr Ile Arg Leu Ser Val Gly Ile Glu Asp Val Thr Asp Leu Ile
 405 410 415

Ala Asp Leu Glu Gln Ala Leu Glu Lys Ile
 420 425

<210> 15

<211> 1173

<212> DNA

<213> *Synechococcus* sp.

<220>

<221> CDS

<222> (1) .. (1173)

<400> 15
 atg tct cag cgt ttc gaa acc ctc cag ctg cat gcc ggc cag tct cca 48
 Met Ser Gln Arg Phe Glu Thr Leu Gln Leu His Ala Gly Gln Ser Pro
 1 5 10 15

gac tcg gcc acc aat gcc aga gcg gtg ccg att tat cag acc agc tcc 96
 Asp Ser Ala Thr Asn Ala Arg Ala Val Pro Ile Tyr Gln Thr Ser Ser
 20 25 30

tac gtc ttc aac gac gcc gag cac ggc gcc aac ctg ttt gga ctg aag 144
 Tyr Val Phe Asn Asp Ala Glu His Gly Ala Asn Leu Phe Gly Leu Lys
 35 40 45

gaa ttc ggc aac atc tac acc cgt ctg atg aac ccg acg acg gat gtg 192
 Glu Phe Gly Asn Ile Tyr Thr Arg Leu Met Asn Pro Thr Thr Asp Val
 50 55 60

ttc gag aag cgg gtg gcg gcc ctg gaa ggg ggt gtg gcc gcg ctg gcc 240
 Phe Glu Lys Arg Val Ala Ala Leu Glu Gly Gly Val Ala Ala Leu Ala
 65 70 75 80

aca gcc tcc ggt cag tcg gct cag ttc ctg gcg atc acg aat tgc atg 288
 Thr Ala Ser Gly Gln Ser Ala Gln Phe Leu Ala Ile Thr Asn Cys Met
 85 90 95

cag gca ggg gat aac ttt gtg tcc acg tcg ttc ctt tac ggc ggc acc 336
 Gln Ala Gly Asp Asn Phe Val Ser Thr Ser Phe Leu Tyr Gly Gly Thr
 100 105 110

tac aac cag ttc aaa gtg caa ttc ccc cgg ctg ggc atc gac gtg cgc 384
 Tyr Asn Gln Phe Lys Val Gln Phe Pro Arg Leu Gly Ile Asp Val Arg
 115 120 125

ttc gct gat ggc gac gac gtg gag agc ttt gct gcg cag atc gac gac 432
 Phe Ala Asp Gly Asp Asp Val Glu Ser Phe Ala Ala Gln Ile Asp Asp
 130 135 140

aaa acc aaa ggc ctc tac gtc gaa gcg atg ggc aat cca cgc ttc aac 480
 Lys Thr Lys Gly Leu Tyr Val Glu Ala Met Gly Asn Pro Arg Phe Asn
 145 150 155 160

atc ccc gat ttc gag ggc ctc tca gcc ctg gct aaa gag cgc ggc atc 528
 Ile Pro Asp Phe Glu Gly Leu Ser Ala Leu Ala Lys Glu Arg Gly Ile
 165 170 175

cca ttg atc gtg gac aac acc ttg gga gct tgc ggt gcc ctg atg cgt 576
 Pro Leu Ile Val Asp Asn Thr Leu Gly Ala Cys Gly Ala Leu Met Arg
 180 185 190

ccg atc gat cat ggc gcg gat gtg gtg gtg gaa agc gcc acc aag tgg 624
 Pro Ile Asp His Gly Ala Asp Val Val Val Glu Ser Ala Thr Lys Trp
 195 200 205

att ggc ggc cat ggc acc agc ctc ggt ggc gtg atc gtt gat gcc ggc 672
 Ile Gly Gly His Gly Thr Ser Leu Gly Gly Val Ile Val Asp Ala Gly
 210 215 220

aca ttt aac tgg ggc aat ggc aaa ttc ccg ctg ctg agc caa ccc agt 720
 Thr Phe Asn Trp Gly Asn Gly Lys Phe Pro Leu Leu Ser Gln Pro Ser
 225 230 235 240

gcg gct tat cac ggc ctt gtg cac tgg gat gcc ttc ggc ttc ggc agc 768
 Ala Ala Tyr His Gly Leu Val His Trp Asp Ala Phe Gly Phe Gly Ser
 245 250 255

gac gtc tgc aag atg ctg gga gtg ccg gac aac cgc aac gtc gcc ttt 816
 Asp Val Cys Lys Met Leu Gly Val Pro Asp Asn Arg Asn Val Ala Phe
 260 265 270

gcc ctg cga gcc cgg gtc gag ggt cta cgg gac tgg ggt ccg gcg gtt 864
 Ala Leu Arg Ala Arg Val Glu Gly Leu Arg Asp Trp Gly Pro Ala Val
 275 280 285

agt ccc ttc aat agc ttc ctg ctg ctg caa ggt cta gaa acc ctc agc 912
 Ser Pro Phe Asn Ser Phe Leu Leu Leu Gln Gly Leu Glu Thr Leu Ser
 290 295 300

ctg cgg gtg gag cgc cac acg gag aac gcc atg gcg ctg gcc acc tgg 960
 Leu Arg Val Glu Arg His Thr Glu Asn Ala Met Ala Leu Ala Thr Trp
 305 310 315 320

cta gca acg cac ccc aat gtg gag cat gtg agc tac cca ggc ctg agc 1008
 Leu Ala Thr His Pro Asn Val Glu His Val Ser Tyr Pro Gly Leu Ser
 325 330 335

agc gat ccg tat cac gca gct gcc aag aaa tac ctg acg ggc cgg ggc 1056
 Ser Asp Pro Tyr His Ala Ala Ala Lys Lys Tyr Leu Thr Gly Arg Gly
 340 345 350

atg gga tgc atg ctg atg ttc tcg ctc aag ggc ggt tac gac gat gca 1104
 Met Gly Cys Met Leu Met Phe Ser Leu Lys Gly Gly Tyr Asp Asp Ala
 355 360 365

gtc cgt ttc atc aac agc ctt caa ctg gcc agt cac ctc gcc aat gtg 1152
 Val Arg Phe Ile Asn Ser Leu Gln Leu Ala Ser His Leu Ala Asn Val
 370 375 380

ggg gat gcc aaa acc tgg tga 1173
 Gly Asp Ala Lys Thr Trp
 385 390

<210> 16

<211> 390

<212> PRT

<213> Synechococcus sp.

<400> 16

Met Ser Gln Arg Phe Glu Thr Leu Gln Leu His Ala Gly Gln Ser Pro
 1 5 10 15

Asp Ser Ala Thr Asn Ala Arg Ala Val Pro Ile Tyr Gln Thr Ser Ser
 20 25 30

Tyr Val Phe Asn Asp Ala Glu His Gly Ala Asn Leu Phe Gly Leu Lys
 35 40 45

Glu Phe Gly Asn Ile Tyr Thr Arg Leu Met Asn Pro Thr Thr Asp Val
 50 55 60

Phe Glu Lys Arg Val Ala Ala Leu Glu Gly Gly Val Ala Ala Leu Ala
 65 70 75 80

Thr Ala Ser Gly Gln Ser Ala Gln Phe Leu Ala Ile Thr Asn Cys Met
 85 90 95

Gln Ala Gly Asp Asn Phe Val Ser Thr Ser Phe Leu Tyr Gly Gly Thr
 100 105 110

Tyr Asn Gln Phe Lys Val Gln Phe Pro Arg Leu Gly Ile Asp Val Arg
 115 120 125

Phe Ala Asp Gly Asp Asp Val Glu Ser Phe Ala Ala Gln Ile Asp Asp
 130 135 140

Lys Thr Lys Gly Leu Tyr Val Glu Ala Met Gly Asn Pro Arg Phe Asn
 145 150 155 160

Ile Pro Asp Phe Glu Gly Leu Ser Ala Leu Ala Lys Glu Arg Gly Ile
 165 170 175

Pro Leu Ile Val Asp Asn Thr Leu Gly Ala Cys Gly Ala Leu Met Arg
 180 185 190

Pro Ile Asp His Gly Ala Asp Val Val Val Glu Ser Ala Thr Lys Trp
 195 200 205

Ile Gly Gly His Gly Thr Ser Leu Gly Gly Val Ile Val Asp Ala Gly
 210 215 220

Thr Phe Asn Trp Gly Asn Gly Lys Phe Pro Leu Leu Ser Gln Pro Ser
 225 230 235 240

Ala Ala Tyr His Gly Leu Val His Trp Asp Ala Phe Gly Phe Gly Ser
 245 250 255

Asp Val Cys Lys Met Leu Gly Val Pro Asp Asn Arg Asn Val Ala Phe
 260 265 270

Ala Leu Arg Ala Arg Val Glu Gly Leu Arg Asp Trp Gly Pro Ala Val
 275 280 285

Ser Pro Phe Asn Ser Phe Leu Leu Leu Gln Gly Leu Glu Thr Leu Ser
 290 295 300

Leu Arg Val Glu Arg His Thr Glu Asn Ala Met Ala Leu Ala Thr Trp
 305 310 315 320

Leu Ala Thr His Pro Asn Val Glu His Val Ser Tyr Pro Gly Leu Ser
 325 330 335

Ser Asp Pro Tyr His Ala Ala Ala Lys Lys Tyr Leu Thr Gly Arg Gly
 340 345 350

Met Gly Cys Met Leu Met Phe Ser Leu Lys Gly Gly Tyr Asp Asp Ala
 355 360 365

Val Arg Phe Ile Asn Ser Leu Gln Leu Ala Ser His Leu Ala Asn Val
 370 375 380

Gly Asp Ala Lys Thr Trp
 385 390

<210> 17

<211> 1314

<212> DNA

<213> Emericella nidulans

<220>

<221> CDS

<222> (1) .. (1314)

<400> 17

atg tcc gac cct tca ccg aaa cgt ttc gag acc ctc cag ctc cat gcg
 Met Ser Asp Pro Ser Pro Lys Arg Phe Glu Thr Leu Gln Leu His Ala
 1 5 10 15

48

ggc cag gag cct gac cct gca act aat tcc cgg gct gtc cca atc tat
 Gly Gln Glu Pro Asp Pro Ala Thr Asn Ser Arg Ala Val Pro Ile Tyr

96

20	25	30	
gcg aca acg tcc tac acc ttc aat gac tcc gca cac ggc gcc agg ctt Ala Thr Thr Ser Tyr Thr Phe Asn Asp Ser Ala His Gly Ala Arg Leu 35 40 45			144
ttt ggc ctc aaa gag ttt ggc aat att tac agc cga att atg aat ccc Phe Gly Leu Lys Glu Phe Gly Asn Ile Tyr Ser Arg Ile Met Asn Pro 50 55 60			192
aca gtc gat gtc ttc gaa aaa cgt att gct gca ctc gag gga ggt gtc Thr Val Asp Val Phe Glu Lys Arg Ile Ala Ala Leu Glu Gly Gly Val 65 70 75 80			240
gct gcg gtg gct gcc tca tct ggc cag gca gcc cag ttc atg gcc atc Ala Ala Val Ala Ala Ser Ser Gly Gln Ala Ala Gln Phe Met Ala Ile 85 90 95			288
tct gct cta gcc cat gct ggt gac aat atc gtt tcc aca agt aat ttg Ser Ala Leu Ala His Ala Gly Asp Asn Ile Val Ser Thr Ser Asn Leu 100 105 110			336
tat ggt ggt aca tac aat cag ttt aag gtc ctt ttc cca cga ctg gga Tyr Gly Gly Thr Tyr Asn Gln Phe Lys Val Leu Phe Pro Arg Leu Gly 115 120 125			384
att acc aca aaa ttc gtg cag gga gac aaa gca gag gac att gcc gcc Ile Thr Thr Lys Phe Val Gln Gly Asp Lys Ala Glu Asp Ile Ala Ala 130 135 140			432
gct atc gat gac cgt acc aag gcc gtc tac gtc gag aca ata gga aac Ala Ile Asp Asp Arg Thr Lys Ala Val Tyr Val Glu Thr Ile Gly Asn 145 150 155 160			480
cct cgc tac aat gtg ccc gac ttt gag gtc att gca aaa gta gcc cat Pro Arg Tyr Asn Val Pro Asp Phe Glu Val Ile Ala Lys Val Ala His 165 170 175			528
gag aag gga att ccc ctt gtg gtt gac aac acc ttc ggt gcc gga ggc Glu Lys Gly Ile Pro Leu Val Val Asp Asn Thr Phe Gly Ala Gly Gly 180 185 190			576
tac ttt gtt cga ccc att gaa cat ggc gcc gac att gtc gtg cac agt Tyr Phe Val Arg Pro Ile Glu His Gly Ala Asp Ile Val Val His Ser 195 200 205			624
gca act aaa tgg att gga ggt cat ggc aca acc atc gga ggc gtt gtc Ala Thr Lys Trp Ile Gly Gly His Gly Thr Thr Ile Gly Gly Val Val 210 215 220			672
gtg gac agc ggc aaa ttc gac tgg ggc aag aac gcc gcg cgg ttt cct Val Asp Ser Gly Lys Phe Asp Trp Gly Lys Asn Ala Ala Arg Phe Pro 225 230 235 240			720
cag ttc acg cag cct tct gaa ggt tac cac ggg ttg aac ttc tgg gag Gln Phe Thr Gln Pro Ser Glu Gly Tyr His Gly Leu Asn Phe Trp Glu 245 250 255			768
acc ttc ggc ccc att gcc ttc gcg att cgt gtc cgg gtc gaa atc ctg Thr Phe Gly Pro Ile Ala Phe Ala Ile Arg Val Arg Val Glu Ile Leu 260 265 270 275 280 285 290			816

260

265

270

cgc gac ctc ggg tcc gcg ctg aac cct ttc gcc gcg cag cag ctc atc 864
 Arg Asp Leu Gly Ser Ala Leu Asn Pro Phe Ala Ala Gln Gln Leu Ile
 275 280 285

ctg ggt ctg gaa acc cta agc ttg cgc gct gag cgt cat gct tcc aac 912
 Leu Gly Leu Glu Thr Leu Ser Leu Arg Ala Glu Arg His Ala Ser Asn
 290 295 300

gct ctg gcc ctc gcc aac tgg cta aag aag aat gat cac gtc agc tgg 960
 Ala Leu Ala Leu Ala Asn Trp Leu Lys Lys Asn Asp His Val Ser Trp
 305 310 315 320

gtt tct tac gtg ggc cta gaa gag cac tcc agc cac gaa gtt gca aag 1008
 Val Ser Tyr Val Gly Leu Glu Glu His Ser Ser His Glu Val Ala Lys
 325 330 335

aag tac ctc aag cgt ggg ttc ggc ggt gtc cta tcc ttt ggt gtc aag 1056
 Lys Tyr Leu Lys Arg Gly Phe Gly Gly Val Leu Ser Phe Gly Val Lys
 340 345 350

ggt gag gca gcc gtc ggt agc cag gtt gtc gac aac ttt aag ctc atc 1104
 Gly Glu Ala Ala Val Gly Ser Gln Val Val Asp Asn Phe Lys Leu Ile
 355 360 365

tcc aat cta gca aat gtt gga gac tcc aag acc ctc gcg att cac ccc 1152
 Ser Asn Leu Ala Asn Val Gly Asp Ser Lys Thr Leu Ala Ile His Pro
 370 375 380

tgg agc acc act cac gag cag ttg acc gac cag gag cga atc gat tct 1200
 Trp Ser Thr Thr His Glu Gln Leu Thr Asp Gln Glu Arg Ile Asp Ser
 385 390 395 400

ggt gtt acg gaa gat gcc atc cgc atc tct gtc ggc act gag cac atc 1248
 Gly Val Thr Glu Asp Ala Ile Arg Ile Ser Val Gly Thr Glu His Ile
 405 410 415

gac gac atc atc gcc gac ttt gaa cag tca ttt gca gcg acc ttc aaa 1296
 Asp Asp Ile Ile Ala Asp Phe Glu Gln Ser Phe Ala Ala Thr Phe Lys
 420 425 430

gtt gtc cgg agt gct tag 1314
 Val Val Arg Ser Ala
 435

<210> 18

<211> 437

<212> PRT

<213> Emericella nidulans

<400> 18

Met Ser Asp Pro Ser Pro Lys Arg Phe Glu Thr Leu Gln Leu His Ala

1 5 10 15
 Gly Gln Glu Pro Asp Pro Ala Thr Asn Ser Arg Ala Val Pro Ile Tyr
 20 25 30
 Ala Thr Thr Ser Tyr Thr Phe Asn Asp Ser Ala His Gly Ala Arg Leu
 35 40 45
 Phe Gly Leu Lys Glu Phe Gly Asn Ile Tyr Ser Arg Ile Met Asn Pro
 50 55 60
 Thr Val Asp Val Phe Glu Lys Arg Ile Ala Ala Leu Glu Gly Gly Val
 65 70 75 80
 Ala Ala Val Ala Ala Ser Ser Gly Gln Ala Ala Gln Phe Met Ala Ile
 85 90 95
 Ser Ala Leu Ala His Ala Gly Asp Asn Ile Val Ser Thr Ser Asn Leu
 100 105 110
 Tyr Gly Gly Thr Tyr Asn Gln Phe Lys Val Leu Phe Pro Arg Leu Gly
 115 120 125
 Ile Thr Thr Lys Phe Val Gln Gly Asp Lys Ala Glu Asp Ile Ala Ala
 130 135 140
 Ala Ile Asp Asp Arg Thr Lys Ala Val Tyr Val Glu Thr Ile Gly Asn
 145 150 155 160
 Pro Arg Tyr Asn Val Pro Asp Phe Glu Val Ile Ala Lys Val Ala His
 165 170 175
 Glu Lys Gly Ile Pro Leu Val Val Asp Asn Thr Phe Gly Ala Gly Gly
 180 185 190
 Tyr Phe Val Arg Pro Ile Glu His Gly Ala Asp Ile Val Val His Ser
 195 200 205
 Ala Thr Lys Trp Ile Gly Gly His Gly Thr Thr Ile Gly Gly Val Val
 210 215 220
 Val Asp Ser Gly Lys Phe Asp Trp Gly Lys Asn Ala Ala Arg Phe Pro
 225 230 235 240

Gln Phe Thr Gln Pro Ser Glu Gly Tyr His Gly Leu Asn Phe Trp Glu
 245 250 255

Thr Phe Gly Pro Ile Ala Phe Ala Ile Arg Val Arg Val Glu Ile Leu
 260 265 270

Arg Asp Leu Gly Ser Ala Leu Asn Pro Phe Ala Ala Gln Gln Leu Ile
 275 280 285

Leu Gly Leu Glu Thr Leu Ser Leu Arg Ala Glu Arg His Ala Ser Asn
 290 295 300

Ala Leu Ala Leu Ala Asn Trp Leu Lys Lys Asn Asp His Val Ser Trp
 305 310 315 320

Val Ser Tyr Val Gly Leu Glu Glu His Ser Ser His Glu Val Ala Lys
 325 330 335

Lys Tyr Leu Lys Arg Gly Phe Gly Gly Val Leu Ser Phe Gly Val Lys
 340 345 350

Gly Glu Ala Ala Val Gly Ser Gln Val Val Asp Asn Phe Lys Leu Ile
 355 360 365

Ser Asn Leu Ala Asn Val Gly Asp Ser Lys Thr Leu Ala Ile His Pro
 370 375 380

Trp Ser Thr Thr His Glu Gln Leu Thr Asp Gln Glu Arg Ile Asp Ser
 385 390 395 400

Gly Val Thr Glu Asp Ala Ile Arg Ile Ser Val Gly Thr Glu His Ile
 405 410 415

Asp Asp Ile Ile Ala Asp Phe Glu Gln Ser Phe Ala Ala Thr Phe Lys
 420 425 430

Val Val Arg Ser Ala
 435

<210> 19

<211> 1287

<212> DNA

<213> Bacteroides fragilis

<220>

<221> CDS

<222> (1)..(1287)

<400> 19

atg gaa acg aaa aaa tta cat ttt gag act tta caa ctc cat gtt gga	48
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1 5 10 15	
cag gag act ccc gac ccg gca acc gat gcg cgt gcc gta cct att tat	96
Gln Glu Thr Pro Asp Pro Ala Thr Asp Ala Arg Ala Val Pro Ile Tyr	
20 25 30	
cag aca act tcc tat gtg ttc cgg gat tcg gcc cat gcc gcc gca cga	144
Gln Thr Thr Ser Tyr Val Phe Arg Asp Ser Ala His Ala Ala Ala Arg	
35 40 45	
ttt gga ttg caa gac cct ggg aat att tat gga cga ctg acc aat tcc	192
Phe Gly Leu Gln Asp Pro Gly Asn Ile Tyr Gly Arg Leu Thr Asn Ser	
50 55 60	
act cag gga gta ttg gag gaa cgc atc gca gca ctt gaa ggg gga gta	240
Thr Gln Gly Val Leu Glu Glu Arg Ile Ala Ala Leu Glu Gly Gly Val	
65 70 75 80	
ggt ggg ctt gcc gtg gct tcc gga gct gct gcc gtg acc tat gct atc	288
Gly Gly Leu Ala Val Ala Ser Gly Ala Ala Ala Val Thr Tyr Ala Ile	
85 90 95	
gag aat atc acc cgt tcc ggt gat cat att gtg gct gcc aag acc att	336
Glu Asn Ile Thr Arg Ser Gly Asp His Ile Val Ala Ala Lys Thr Ile	
100 105 110	
tat ggg ggc aca tat aac ttg ctg gcg cat act ctg cct gct tat gga	384
Tyr Gly Gly Thr Tyr Asn Leu Leu Ala His Thr Leu Pro Ala Tyr Gly	
115 120 125	
gta acg acc act ttt gta gat ccg tcc gat ctt ttt aat ttc gaa cgg	432
Val Thr Thr Thr Phe Val Asp Pro Ser Asp Leu Phe Asn Phe Glu Arg	
130 135 140	
gcg att cgt gaa aat aca aag gcg ata ttc att gaa act ctg gga aac	480
Ala Ile Arg Glu Asn Thr Lys Ala Ile Phe Ile Glu Thr Leu Gly Asn	
145 150 155 160	
ccc aat tcc aat att atc gat atg gat gcc gta gct gcc att gcc cat	528
Pro Asn Ser Asn Ile Ile Asp Met Asp Ala Val Ala Ala Ile Ala His	
165 170 175	
aaa tat cgg att ccg ctg att gtg gat aat act ttc ggt acg cct tac	576
Lys Tyr Arg Ile Pro Leu Ile Val Asp Asn Thr Phe Gly Thr Pro Tyr	
180 185 190	

ctt atc cgt ccc att gag cac ggg gca gac att gtg gta cat tct gcc Leu Ile Arg Pro Ile Glu His Gly Ala Asp Ile Val Val His Ser Ala 195 200 205	624
aca aaa ttc att ggc gga cac ggc agt tcg ttg gga gga gtt att gtc Thr Lys Phe Ile Gly Gly His Gly Ser Ser Leu Gly Gly Val Ile Val 210 215 220	672
gat tcc ggt aaa ttt gac tgg gtt gct tcc ggt aaa ttc ccg caa ctg Asp Ser Gly Lys Phe Asp Trp Val Ala Ser Gly Lys Phe Pro Gln Leu 225 230 235 240	720
acc gag ccg gat gca agt tat cat ggg gta cgg ttt gtc gat gct gcc Thr Glu Pro Asp Ala Ser Tyr His Gly Val Arg Phe Val Asp Ala Ala 245 250 255	768
ggg gct gct gcc tac att gtc cgt ata cgt gcc gtg ttg ctg cgc gat Gly Ala Ala Ala Tyr Ile Val Arg Ile Arg Ala Val Leu Leu Arg Asp 260 265 270	816
acg ggt gct gcc atc agc ccg ttc aat gct ttt atc ttg ctg caa ggg Thr Gly Ala Ala Ile Ser Pro Phe Asn Ala Phe Ile Leu Leu Gln Gly 275 280 285	864
ttg gag act ttg tct ttg cgt gta gaa cgg cat gtg gcc aat gct ttg Leu Glu Thr Leu Ser Leu Arg Val Glu Arg His Val Ala Asn Ala Leu 290 295 300	912
aag gtt att gat ttt ctg gtg aac cat ccg aag gta gcg gct gtt aat Lys Val Ile Asp Phe Leu Val Asn His Pro Lys Val Ala Ala Val Asn 305 310 315 320	960
cat cca tca ttg ccc ggt cat ccg gat cat gcc atc tat caa cgt tat His Pro Ser Leu Pro Gly His Pro Asp His Ala Ile Tyr Gln Arg Tyr 325 330 335	1008
ttt cct ggc ggg gca ggt tct atc ttc act ttc gag gta aag gga gga Phe Pro Gly Gly Ala Gly Ser Ile Phe Thr Phe Glu Val Lys Gly Gly 340 345 350	1056
acg gag gaa gcg cag aag ttt atc gat agt ctg cag ata ttc tct ttg Thr Glu Glu Ala Gln Lys Phe Ile Asp Ser Leu Gln Ile Phe Ser Leu 355 360 365	1104
ctg gcc aat gtg gcc gat gtg aag tcg ctg gtg att cat ccg ggc act Leu Ala Asn Val Ala Asp Val Lys Ser Leu Val Ile His Pro Gly Thr 370 375 380	1152
acc aca cac tcg cag ttg aat gcg cag gag ctg gag gaa cag ggg att Thr Thr His Ser Gln Leu Asn Ala Gln Glu Leu Glu Glu Gln Gly Ile 385 390 395 400	1200
aaa ccc gga acg gtc aga ctt tcg ata ggt acg gag cat att gag gac Lys Pro Gly Thr Val Arg Leu Ser Ile Gly Thr Glu His Ile Glu Asp 405 410 415	1248
att att gat gac tta cgt cag gca tta gag aaa att taa Ile Ile Asp Asp Leu Arg Gln Ala Leu Glu Lys Ile 420 425	1287

<210> 20

<211> 428

<212> PRT

<213> Bacteroides fragilis

<400> 20

Met Glu Thr Lys Lys Leu His Phe Glu Thr Leu Gln Leu His Val Gly
1 5 10 15

Gln Glu Thr Pro Asp Pro Ala Thr Asp Ala Arg Ala Val Pro Ile Tyr
20 25 30

Gln Thr Thr Ser Tyr Val Phe Arg Asp Ser Ala His Ala Ala Ala Arg
35 40 45

Phe Gly Leu Gln Asp Pro Gly Asn Ile Tyr Gly Arg Leu Thr Asn Ser
50 55 60

Thr Gln Gly Val Leu Glu Glu Arg Ile Ala Ala Leu Glu Gly Gly Val
65 70 75 80

Gly Gly Leu Ala Val Ala Ser Gly Ala Ala Ala Val Thr Tyr Ala Ile
85 90 95

Glu Asn Ile Thr Arg Ser Gly Asp His Ile Val Ala Ala Lys Thr Ile
100 105 110

Tyr Gly Gly Thr Tyr Asn Leu Leu Ala His Thr Leu Pro Ala Tyr Gly
115 120 125

Val Thr Thr Thr Phe Val Asp Pro Ser Asp Leu Phe Asn Phe Glu Arg
130 135 140

Ala Ile Arg Glu Asn Thr Lys Ala Ile Phe Ile Glu Thr Leu Gly Asn
145 150 155 160

Pro Asn Ser Asn Ile Ile Asp Met Asp Ala Val Ala Ala Ile Ala His
165 170 175

Lys Tyr Arg Ile Pro Leu Ile Val Asp Asn Thr Phe Gly Thr Pro Tyr
180 185 190

Leu Ile Arg Pro Ile Glu His Gly Ala Asp Ile Val Val His Ser Ala
195 200 205

Thr Lys Phe Ile Gly Gly His Gly Ser Ser Leu Gly Gly Val Ile Val
210 215 220

Asp Ser Gly Lys Phe Asp Trp Val Ala Ser Gly Lys Phe Pro Gln Leu
225 230 235 240

Thr Glu Pro Asp Ala Ser Tyr His Gly Val Arg Phe Val Asp Ala Ala
245 250 255

Gly Ala Ala Ala Tyr Ile Val Arg Ile Arg Ala Val Leu Leu Arg Asp
260 265 270

Thr Gly Ala Ala Ile Ser Pro Phe Asn Ala Phe Ile Leu Leu Gln Gly
275 280 285

Leu Glu Thr Leu Ser Leu Arg Val Glu Arg His Val Ala Asn Ala Leu
290 295 300

Lys Val Ile Asp Phe Leu Val Asn His Pro Lys Val Ala Ala Val Asn
305 310 315 320

His Pro Ser Leu Pro Gly His Pro Asp His Ala Ile Tyr Gln Arg Tyr
325 330 335

Phe Pro Gly Gly Ala Gly Ser Ile Phe Thr Phe Glu Val Lys Gly Gly
340 345 350

Thr Glu Glu Ala Gln Lys Phe Ile Asp Ser Leu Gln Ile Phe Ser Leu
355 360 365

Leu Ala Asn Val Ala Asp Val Lys Ser Leu Val Ile His Pro Gly Thr
370 375 380

Thr Thr His Ser Gln Leu Asn Ala Gln Glu Leu Glu Glu Gln Gly Ile
385 390 395 400

Lys Pro Gly Thr Val Arg Leu Ser Ile Gly Thr Glu His Ile Glu Asp
405 410 415

Ile Ile Asp Asp Leu Arg Gln Ala Leu Glu Lys Ile
420 425

<210> 21

<211> 1278

<212> DNA

<213> *Pseudomonas aeruginosa*

<220>

<221> CDS

<222> (1) .. (1278)

<400> 21

atg aaa ctg gaa acc ctg gcc gtc cac gcc ggc tac agc cct gac ccg	48
Met Lys Leu Glu Thr Leu Ala Val His Ala Gly Tyr Ser Pro Asp Pro	
1 5 10 15	
acc acc cgc gcg gtg gcg gtg ccg atc tac cag acc acc tcc tac gcc	96
Thr Thr Arg Ala Val Ala Val Pro Ile Tyr Gln Thr Thr Ser Tyr Ala	
20 25 30	
ttc gac gac acc cag cat ggc gcc gac ctg ttc gac ctg aag gta ccg	144
Phe Asp Asp Thr Gln His Gly Ala Asp Leu Phe Asp Leu Lys Val Pro	
35 40 45	
ggc aac atc tac aca cgg atc atg aac ccc acc aac gac gta ctg gaa	192
Gly Asn Ile Tyr Thr Arg Ile Met Asn Pro Thr Asn Asp Val Leu Glu	
50 55 60	
cag cgc gtc gcg gcg ctg gaa ggc ggg gtc ggg gcg ctg gcg gtg gcc	240
Gln Arg Val Ala Ala Leu Glu Gly Gly Val Gly Ala Leu Ala Val Ala	
65 70 75 80	
tcg ggg atg gcg gcc atc acc tac gcg atc cag acc gtc gcc gag gcc	288
Ser Gly Met Ala Ala Ile Thr Tyr Ala Ile Gln Thr Val Ala Glu Ala	
85 90 95	
ggc gac aac atc gtc tcg gtg gcc aag ctc tac ggc ggc acc tac aac	336
Gly Asp Asn Ile Val Ser Val Ala Lys Leu Tyr Gly Gly Thr Tyr Asn	
100 105 110	
ctg ctg gcc cac acc ctg cca cgc atc ggc atc cag gcg cgc ttc gcc	384
Leu Leu Ala His Thr Leu Pro Arg Ile Gly Ile Gln Ala Arg Phe Ala	
115 120 125	
gcc cac gac gac gtc gcc gcc ctg gaa gcg ctg atc gac gag cgg acc	432
Ala His Asp Asp Val Ala Ala Leu Glu Ala Leu Ile Asp Glu Arg Thr	
130 135 140	
aag gcc gtg ttc tgc gaa acc atc ggc aac ccg gcg ggc aac atc atc	480
Lys Ala Val Phe Cys Glu Thr Ile Gly Asn Pro Ala Gly Asn Ile Ile	
145 150 155 160	

gac ctg cag gca ctg gcc gac gcc gct cac cgc cac ggc gtg cca ctg	528
Asp Leu Gln Ala Leu Ala Asp Ala Ala His Arg His Gly Val Pro Leu	
165 170 175	
atc gtc gac aac acg gta gcc acc ccg gtg ctc tgc cgg ccg ttc gag	576
Ile Val Asp Asn Thr Val Ala Thr Pro Val Leu Cys Arg Pro Phe Glu	
180 185 190	
cac ggc gcc gac atc gtc gtg cac tcg ctg acc aag tac atg ggc ggc	624
His Gly Ala Asp Ile Val Val His Ser Leu Thr Lys Tyr Met Gly Gly	
195 200 205	
cac ggc acc agc atc ggc ggg atc gtg gtc gac tcc ggc aaa ttc gac	672
His Gly Thr Ser Ile Gly Gly Ile Val Val Asp Ser Gly Lys Phe Asp	
210 215 220	
tgg gcg gcg aac aag tcg cgc ttc ccg ctg ctg aac acg ccc gat ccg	720
Trp Ala Ala Asn Lys Ser Arg Phe Pro Leu Leu Asn Thr Pro Asp Pro	
225 230 235 240	
tcc tac cac ggc gtc acc tac acc gag gcc ttc gga ccc gcc gcc ttc	768
Ser Tyr His Gly Val Thr Tyr Thr Glu Ala Phe Gly Pro Ala Ala Phe	
245 250 255	
atc ggc cgc tgc cgg gtg gta ccg ctg cgc aac atg ggc gcg gcg ctc	816
Ile Gly Arg Cys Arg Val Val Pro Leu Arg Asn Met Gly Ala Ala Leu	
260 265 270	
tcg ccg ttc aac gcc ttc ctc atc ctc caa ggc ctg gag acc ctg gcg	864
Ser Pro Phe Asn Ala Phe Leu Ile Leu Gln Gly Leu Glu Thr Leu Ala	
275 280 285	
ctg cgc atg gag cgc cac tgc gac aac gcc ctc gcc gtg gcc cgc tac	912
Leu Arg Met Glu Arg His Cys Asp Asn Ala Leu Ala Val Ala Arg Tyr	
290 295 300	
ctg cag cag cat ccg cag gtg gcc tgg gtg aaa tac gcc ggc ctc gcc	960
Leu Gln Gln His Pro Gln Val Ala Trp Val Lys Tyr Ala Gly Leu Ala	
305 310 315 320	
gac aac ccc gag cac gcc ctg gcc ccg cgc tac ctg ggg ggc cgc ccg	1008
Asp Asn Pro Glu His Ala Leu Ala Arg Arg Tyr Leu Gly Gly Arg Pro	
325 330 335	
gcg gcg atc ctg tct ttc ggc atc cag ggc ggc agc gcc gcc ggc gcg	1056
Ala Ala Ile Leu Ser Phe Gly Ile Gln Gly Gly Ser Ala Ala Gly Ala	
340 345 350	
cgc ttc atc gac gcc ttg aag ctg gtg gtg ccg ctg gtc aac atc ggc	1104
Arg Phe Ile Asp Ala Leu Lys Leu Val Val Arg Leu Val Asn Ile Gly	
355 360 365	
gac gcc aag tcc ctg gcc tgc cac ccg gcg agc acc acc cac cgc cag	1152
Asp Ala Lys Ser Leu Ala Cys His Pro Ala Ser Thr Thr His Arg Gln	
370 375 380	
ttg aac gcg gag gaa ctg gcc cgc gcc gga gtc tcc gac gac atg gtg	1200
Leu Asn Ala Glu Glu Leu Ala Arg Ala Gly Val Ser Asp Asp Met Val	
385 390 395 400	

cgg ctg tcg atc ggc atc gag cac atc gac gac atc ctc gcc gac ctc 1248
 Arg Leu Ser Ile Gly Ile Glu His Ile Asp Asp Ile Leu Ala Asp Leu
 405 410 415

gac cag gcc ctg gcc gcc gcc gca cgc tga 1278
 Asp Gln Ala Leu Ala Ala Ala Arg
 420 425

<210> 22

<211> 425

<212> PRT

<213> Pseudomonas aeruginosa

<400> 22

Met Lys Leu Glu Thr Leu Ala Val His Ala Gly Tyr Ser Pro Asp Pro
 1 5 10 15

Thr Thr Arg Ala Val Ala Val Pro Ile Tyr Gln Thr Thr Ser Tyr Ala
 20 25 30

Phe Asp Asp Thr Gln His Gly Ala Asp Leu Phe Asp Leu Lys Val Pro
 35 40 45

Gly Asn Ile Tyr Thr Arg Ile Met Asn Pro Thr Asn Asp Val Leu Glu
 50 55 60

Gln Arg Val Ala Ala Leu Glu Gly Gly Val Gly Ala Leu Ala Val Ala
 65 70 75 80

Ser Gly Met Ala Ala Ile Thr Tyr Ala Ile Gln Thr Val Ala Glu Ala
 85 90 95

Gly Asp Asn Ile Val Ser Val Ala Lys Leu Tyr Gly Gly Thr Tyr Asn
 100 105 110

Leu Leu Ala His Thr Leu Pro Arg Ile Gly Ile Gln Ala Arg Phe Ala
 115 120 125

Ala His Asp Asp Val Ala Ala Leu Glu Ala Leu Ile Asp Glu Arg Thr
 130 135 140

Lys Ala Val Phe Cys Glu Thr Ile Gly Asn Pro Ala Gly Asn Ile Ile
 145 150 155 160

Asp Leu Gln Ala Leu Ala Asp Ala Ala His Arg His Gly Val Pro Leu
 165 170 175

Ile Val Asp Asn Thr Val Ala Thr Pro Val Leu Cys Arg Pro Phe Glu
 180 185 190

His Gly Ala Asp Ile Val Val His Ser Leu Thr Lys Tyr Met Gly Gly
 195 200 205

His Gly Thr Ser Ile Gly Gly Ile Val Val Asp Ser Gly Lys Phe Asp
 210 215 220

Trp Ala Ala Asn Lys Ser Arg Phe Pro Leu Leu Asn Thr Pro Asp Pro
 225 230 235 240

Ser Tyr His Gly Val Thr Tyr Thr Glu Ala Phe Gly Pro Ala Ala Phe
 245 250 255

Ile Gly Arg Cys Arg Val Val Pro Leu Arg Asn Met Gly Ala Ala Leu
 260 265 270

Ser Pro Phe Asn Ala Phe Leu Ile Leu Gln Gly Leu Glu Thr Leu Ala
 275 280 285

Leu Arg Met Glu Arg His Cys Asp Asn Ala Leu Ala Val Ala Arg Tyr
 290 295 300

Leu Gln Gln His Pro Gln Val Ala Trp Val Lys Tyr Ala Gly Leu Ala
 305 310 315 320

Asp Asn Pro Glu His Ala Leu Ala Arg Arg Tyr Leu Gly Gly Arg Pro
 325 330 335

Ala Ala Ile Leu Ser Phe Gly Ile Gln Gly Gly Ser Ala Ala Gly Ala
 340 345 350

Arg Phe Ile Asp Ala Leu Lys Leu Val Val Arg Leu Val Asn Ile Gly
 355 360 365

Asp Ala Lys Ser Leu Ala Cys His Pro Ala Ser Thr Thr His Arg Gln
 370 375 380

Leu Asn Ala Glu Glu Leu Ala Arg Ala Gly Val Ser Asp Asp Met Val
 385 390 395 400

Arg Leu Ser Ile Gly Ile Glu His Ile Asp Asp Ile Leu Ala Asp Leu
 405 410 415

Asp Gln Ala Leu Ala Ala Ala Arg
 420 425

<210> 23

<211> 1296

<212> DNA

<213> Bordetella bronchiseptica

<220>

<221> CDS

<222> (1) .. (1296)

<400> 23

atg agc gaa ccg aac caa ccc atc tgg cgg ctg gag acc atc gcc gta	48
Met Ser Glu Pro Asn Gln Pro Ile Trp Arg Leu Glu Thr Ile Ala Val	
1 5 10 15	
cat ggg ggc tac cgg ccc gac ccg acc acg cgc gcg gtg gcg gtg ccg	96
His Gly Gly Tyr Arg Pro Asp Pro Thr Thr Arg Ala Val Ala Val Pro	
20 25 30	
atc tac cag acc gtg gcc tat gcg ttc gac gac acc cag cat ggc gcg	144
Ile Tyr Gln Thr Val Ala Tyr Ala Phe Asp Asp Thr Gln His Gly Ala	
35 40 45	
gac ctg ttc gac ctg aag gtg ccg ggc aat atc tac acc cgc atc atg	192
Asp Leu Phe Asp Leu Lys Val Pro Gly Asn Ile Tyr Thr Arg Ile Met	
50 55 60	
aac ccc acc acc gac gtg ctg gag cag cgc gtg gcg gcg ctg gaa tgc	240
Asn Pro Thr Thr Asp Val Leu Glu Gln Arg Val Ala Ala Leu Glu Cys	
65 70 75 80	
ggc gtg gcc gcg ctg gcg ctg gcc tcc ggc cag gcg gcg gtg acc tat	288
Gly Val Ala Ala Leu Ala Leu Ala Ser Gly Gln Ala Ala Val Thr Tyr	
85 90 95	
gcg atc ctg acc atc gcc gag gcg ggc gac aac atc gtg tcc tcc agc	336
Ala Ile Leu Thr Ile Ala Glu Ala Gly Asp Asn Ile Val Ser Ser Ser	
100 105 110	
acg ctg tat ggc ggc acg tac aac ctg ttc gcc cac acg ctg ccg cag	384
Thr Leu Tyr Gly Gly Thr Tyr Asn Leu Phe Ala His Thr Leu Pro Gln	
115 120 125	

tac ggc atc acg acc cgc ttc gcc gat ccg cgc aac ctg gct tcg ttc Tyr Gly Ile Thr Thr Arg Phe Ala Asp Pro Arg Asn Leu Ala Ser Phe 130 135 140	432
gag gcg ctg atc gac gag cgc acc aag gcc att ttc gcc gag tcg gtg Glu Ala Leu Ile Asp Glu Arg Thr Lys Ala Ile Phe Ala Glu Ser Val 145 150 155 160	480
ggc aat ccg ctg ggc aac gtc acc gac atc gcc gcg ctg gcc gag atc Gly Asn Pro Leu Gly Asn Val Thr Asp Ile Ala Ala Leu Ala Glu Ile 165 170 175	528
gcg cac cgc cat ggc gtg ccg ctg atc gtc gac aac acg gtg ccg tcg Ala His Arg His Gly Val Pro Leu Ile Val Asp Asn Thr Val Pro Ser 180 185 190	576
ccc tac ctg ctg cgc ccc atc gag cac ggc gcc gac atc gtg gtg cag Pro Tyr Leu Leu Arg Pro Ile Glu His Gly Ala Asp Ile Val Val Gln 195 200 205	624
tcg ctc acc aag tac ctg ggc ggg cac ggc acc agc ctg ggc ggg gcc Ser Leu Thr Lys Tyr Leu Gly Gly His Gly Thr Ser Leu Gly Gly Ala 210 215 220	672
atc atc gat tcg ggc aag ttt ccc tgg gcc gag cac aag gcg cgc ttc Ile Ile Asp Ser Gly Lys Phe Pro Trp Ala Glu His Lys Ala Arg Phe 225 230 235 240	720
aag cgc ctg aac gag ccc gac gtg agc tac cac ggc gtg gtc tac acc Lys Arg Leu Asn Glu Pro Asp Val Ser Tyr His Gly Val Val Tyr Thr 245 250 255	768
gag gcg ttc ggc gcg gcg gcc tat atc ggc cgc gcc cgc gtg gtg ccg Glu Ala Phe Gly Ala Ala Ala Tyr Ile Gly Arg Ala Arg Val Val Pro 260 265 270	816
ctg cgc aat acc ggc gcg gcc att tcg ccg ttc aac gcc ttc cag atc Leu Arg Asn Thr Gly Ala Ala Ile Ser Pro Phe Asn Ala Phe Gln Ile 275 280 285	864
ctg cag ggc atc gag acg ctg gcg ctg cgc gtg gac cgc atc gtc gag Leu Gln Gly Ile Glu Thr Leu Ala Leu Arg Val Asp Arg Ile Val Glu 290 295 300	912
aac tcg gtc aag gtg gcc ggg ttc ctg cgc gac cat ccc aag gtc gaa Asn Ser Val Lys Val Ala Gly Phe Leu Arg Asp His Pro Lys Val Glu 305 310 315 320	960
tgg gtc aac tat gcc ggc ctg ccc gac cat gcc gac cat gcg ctg gtg Trp Val Asn Tyr Ala Gly Leu Pro Asp His Ala Asp His Ala Leu Val 325 330 335	1008
cgc aag tac atg ggc ggc aag gcc ccc ggc ctg ttc act ttc ggc gtg Arg Lys Tyr Met Gly Gly Lys Ala Pro Gly Leu Phe Thr Phe Gly Val 340 345 350	1056
aag ggc ggc cgc gag gcc ggc gcg cgc ttc cag gac gcc ttg cag ctg Lys Gly Gly Arg Glu Ala Gly Ala Arg Phe Gln Asp Ala Leu Gln Leu 355 360 365	1104

ttc acc cgc ctg gtg aac atc ggc gac gcc aag tcg ctg gcc acg cac 1152
 Phe Thr Arg Leu Val Asn Ile Gly Asp Ala Lys Ser Leu Ala Thr His
 370 375 380

cgc gct tcc acc acg cac cgc cag ctc aac ccc gaa gag ctc gaa aag 1200
 Pro Ala Ser Thr Thr His Arg Gln Leu Asn Pro Glu Glu Leu Glu Lys
 385 390 395 400

gcc ggc gtg cgc gag gaa acg gtg cgc ctg tcg atc ggg atc gag cat 1248
 Ala Gly Val Arg Glu Glu Thr Val Arg Leu Ser Ile Gly Ile Glu His
 405 410 415

atc gac gac ctg atc gcc gac ctg gaa cag gcg ctg gcg caa gtc tga 1296
 Ile Asp Asp Leu Ile Ala Asp Leu Glu Gln Ala Leu Ala Gln Val
 420 425 430

<210> 24

<211> 431

<212> PRT

<213> Bordetella bronchiseptica

<400> 24

Met Ser Glu Pro Asn Gln Pro Ile Trp Arg Leu Glu Thr Ile Ala Val
 1 5 10 15

His Gly Gly Tyr Arg Pro Asp Pro Thr Thr Arg Ala Val Ala Val Pro
 20 25 30

Ile Tyr Gln Thr Val Ala Tyr Ala Phe Asp Asp Thr Gln His Gly Ala
 35 40 45

Asp Leu Phe Asp Leu Lys Val Pro Gly Asn Ile Tyr Thr Arg Ile Met
 50 55 60

Asn Pro Thr Thr Asp Val Leu Glu Gln Arg Val Ala Ala Leu Glu Cys
 65 70 75 80

Gly Val Ala Ala Leu Ala Leu Ala Ser Gly Gln Ala Ala Val Thr Tyr
 85 90 95

Ala Ile Leu Thr Ile Ala Glu Ala Gly Asp Asn Ile Val Ser Ser Ser
 100 105 110

Thr Leu Tyr Gly Gly Thr Tyr Asn Leu Phe Ala His Thr Leu Pro Gln
 115 120 125

Tyr Gly Ile Thr Thr Arg Phe Ala Asp Pro Arg Asn Leu Ala Ser Phe
 130 135 140

Glu Ala Leu Ile Asp Glu Arg Thr Lys Ala Ile Phe Ala Glu Ser Val
 145 150 155 160

Gly Asn Pro Leu Gly Asn Val Thr Asp Ile Ala Ala Leu Ala Glu Ile
 165 170 175

Ala His Arg His Gly Val Pro Leu Ile Val Asp Asn Thr Val Pro Ser
 180 185 190

Pro Tyr Leu Leu Arg Pro Ile Glu His Gly Ala Asp Ile Val Val Gln
 195 200 205

Ser Leu Thr Lys Tyr Leu Gly Gly His Gly Thr Ser Leu Gly Gly Ala
 210 215 220

Ile Ile Asp Ser Gly Lys Phe Pro Trp Ala Glu His Lys Ala Arg Phe
 225 230 235 240

Lys Arg Leu Asn Glu Pro Asp Val Ser Tyr His Gly Val Val Tyr Thr
 245 250 255

Glu Ala Phe Gly Ala Ala Ala Tyr Ile Gly Arg Ala Arg Val Val Pro
 260 265 270

Leu Arg Asn Thr Gly Ala Ala Ile Ser Pro Phe Asn Ala Phe Gln Ile
 275 280 285

Leu Gln Gly Ile Glu Thr Leu Ala Leu Arg Val Asp Arg Ile Val Glu
 290 295 300

Asn Ser Val Lys Val Ala Gly Phe Leu Arg Asp His Pro Lys Val Glu
 305 310 315 320

Trp Val Asn Tyr Ala Gly Leu Pro Asp His Ala Asp His Ala Leu Val
 325 330 335

Arg Lys Tyr Met Gly Gly Lys Ala Pro Gly Leu Phe Thr Phe Gly Val
 340 345 350

Lys Gly Gly Arg Glu Ala Gly Ala Arg Phe Gln Asp Ala Leu Gln Leu
 355 360 365

Phe Thr Arg Leu Val Asn Ile Gly Asp Ala Lys Ser Leu Ala Thr His
 370 375 380

Pro Ala Ser Thr Thr His Arg Gln Leu Asn Pro Glu Glu Leu Glu Lys
 385 390 395 400

Ala Gly Val Arg Glu Glu Thr Val Arg Leu Ser Ile Gly Ile Glu His
 405 410 415

Ile Asp Asp Leu Ile Ala Asp Leu Glu Gln Ala Leu Ala Gln Val
 420 425 430

<210> 25

<211> 1269

<212> DNA

<213> Nitrosomonas europaea

<220>

<221> CDS

<222> (1) .. (1269)

<400> 25
 atg aaa cgg gaa aca ctc gcc att cat ggc ggt ttt gcc ggc gat ccg 48
 Met Lys Arg Glu Thr Leu Ala Ile His Gly Gly Phe Ala Gly Asp Pro
 1 5 10 15

cag act cat gca gtc gcg gtc ccc att tac cag acc acc agc tac tat 96
 Gln Thr His Ala Val Ala Val Pro Ile Tyr Gln Thr Thr Ser Tyr Tyr
 20 25 30

ttt gat gat act cag cac ggg gct gat ttg ttt gat ctg aag gtg cag 144
 Phe Asp Asp Thr Gln His Gly Ala Asp Leu Phe Asp Leu Lys Val Gln
 35 40 45

ggt aac atc tac aca cgc atc atg aac ccg act act gct gtc ctg gaa 192
 Gly Asn Ile Tyr Thr Arg Ile Met Asn Pro Thr Thr Ala Val Leu Glu
 50 55 60

gaa aga gtg gcg tta ctg gaa gga gga gtg gga gcg ctg gcc atg gct 240
 Glu Arg Val Ala Leu Leu Glu Gly Gly Val Gly Ala Leu Ala Met Ala
 65 70 75 80

tcc ggc atg gcc gcc att aca gcc tgt gtg cag act ctg gcc agg gcg 288
 Ser Gly Met Ala Ala Ile Thr Ala Cys Val Gln Thr Leu Ala Arg Ala

85	90	95	
ggc gac aac att atc tcc acc agc cag gtt tac ggt ggc acc tat aat Gly Asp Asn Ile Ile Ser Thr Ser Gln Val Tyr Gly Gly Thr Tyr Asn 100 105 110			336
ttc ttt tgc cat acg ttg ccc aat ctg ggt att gaa gtt cgc atg gtg Phe Phe Cys His Thr Leu Pro Asn Leu Gly Ile Glu Val Arg Met Val 115 120 125			384
gat ggt cgt aat ccg gcc gct ttt gcc gat gcc atc gat gac aat acc Asp Gly Arg Asn Pro Ala Ala Phe Ala Asp Ala Ile Asp Asp Asn Thr 130 135 140			432
aga atg att tat tgc gag tcg atc gga aat ccg gcc ggt aat gtg gtg Arg Met Ile Tyr Cys Glu Ser Ile Gly Asn Pro Ala Gly Asn Val Val 145 150 155 160			480
gat atc gcc gca ctg gct gaa gtg gcg cat gca gcg ggc gtg ccg ctg Asp Ile Ala Ala Leu Ala Glu Val Ala His Ala Ala Gly Val Pro Leu 165 170 175			528
gta gtg gac aat acc gta cca acc ccg gtg ctt tgt cgt cct ttc gaa Val Val Asp Asn Thr Val Pro Thr Pro Val Leu Cys Arg Pro Phe Glu 180 185 190			576
cat ggt gcc gat atc gtc gtc cat gcg ctg acc aaa tac atg ggt ggt His Gly Ala Asp Ile Val Val His Ala Leu Thr Lys Tyr Met Gly Gly 195 200 205			624
cac ggc acc agc atc ggc gga atc atc gtg gat tcc ggc aag ttc ccc His Gly Thr Ser Ile Gly Gly Ile Ile Val Asp Ser Gly Lys Phe Pro 210 215 220			672
tgg gaa ggc aac tcg cgt ttt cca caa ttc aac caa cct gat ccc agc Trp Glu Gly Asn Ser Arg Phe Pro Gln Phe Asn Gln Pro Asp Pro Ser 225 230 235 240			720
tat cac ggt gtg gtt tat gtg gat gca ttt ggt ccg gct gcg ttt atc Tyr His Gly Val Val Tyr Val Asp Ala Phe Gly Pro Ala Ala Phe Ile 245 250 255			768
ggc cgt gcg cgt gtg gta ccg ttg cgc aac atg gga gcg gca att tca Gly Arg Ala Arg Val Val Pro Leu Arg Asn Met Gly Ala Ala Ile Ser 260 265 270			816
cct ttc aat tct ttt ctg att ctg caa ggt atc gaa acc ctg ccg ttg Pro Phe Asn Ser Phe Leu Ile Leu Gln Gly Ile Glu Thr Leu Pro Leu 275 280 285			864
agg atg gaa cgg cat tgc acc aat gcg ctg gcg att gca cgt tat ctg Arg Met Glu Arg His Cys Thr Asn Ala Leu Ala Ile Ala Arg Tyr Leu 290 295 300			912
caa agg cat ccc aaa gtc agc tgg gtc aat ttt gcc ggc ctt gaa gat Gln Arg His Pro Lys Val Ser Trp Val Asn Phe Ala Gly Leu Glu Asp 305 310 315 320			960
aac cgt gat tac gca ctg gtg cag aaa tac atg gat ggc ggt att ccc Asn Arg Asp Tyr Ala Leu Val Gln Lys Tyr Met Asp Gly Gly Ile Pro			1008

325

330

335

tca tcg att ctg agt ttt ggc atc aag ggc ggg cgc gag gct tgt gct 1056
 Ser Ser Ile Leu Ser Phe Gly Ile Lys Gly Gly Arg Glu Ala Cys Ala
 340 345 350

cgc ttt atg gac aga ctg atg ctg atc aaa cgg ctg gtc aac atc ggg 1104
 Arg Phe Met Asp Arg Leu Met Leu Ile Lys Arg Leu Val Asn Ile Gly
 355 360 365

gat gcc aaa acg ctg gcc tgc cac ccg gcg acg acc acc cac cgt cag 1152
 Asp Ala Lys Thr Leu Ala Cys His Pro Ala Thr Thr Thr His Arg Gln
 370 375 380

ctc aat gat gaa gaa ctg gca aaa gcc ggt gtc agt gct gat ctg gtg 1200
 Leu Asn Asp Glu Glu Leu Ala Lys Ala Gly Val Ser Ala Asp Leu Val
 385 390 395 400

cgt tta tgt gtc ggc atc gag cat att gac gat ctg att gcc gat gta 1248
 Arg Leu Cys Val Gly Ile Glu His Ile Asp Asp Leu Ile Ala Asp Val
 405 410 415

gag cag gct ttc cag gat tag 1269
 Glu Gln Ala Phe Gln Asp
 420

<210> 26

<211> 422

<212> PRT

<213> Nitrosomonas europaea

<400> 26

Met Lys Arg Glu Thr Leu Ala Ile His Gly Gly Phe Ala Gly Asp Pro
 1 5 10 15

Gln Thr His Ala Val Ala Val Pro Ile Tyr Gln Thr Thr Ser Tyr Tyr
 20 25 30

Phe Asp Asp Thr Gln His Gly Ala Asp Leu Phe Asp Leu Lys Val Gln
 35 40 45

Gly Asn Ile Tyr Thr Arg Ile Met Asn Pro Thr Thr Ala Val Leu Glu
 50 55 60

Glu Arg Val Ala Leu Leu Glu Gly Gly Val Gly Ala Leu Ala Met Ala
 65 70 75 80

Ser Gly Met Ala Ala Ile Thr Ala Cys Val Gln Thr Leu Ala Arg Ala

85

90

95

Gly Asp Asn Ile Ile Ser Thr Ser Gln Val Tyr Gly Gly Thr Tyr Asn
 100 105 110

Phe Phe Cys His Thr Leu Pro Asn Leu Gly Ile Glu Val Arg Met Val
 115 120 125

Asp Gly Arg Asn Pro Ala Ala Phe Ala Asp Ala Ile Asp Asp Asn Thr
 130 135 140

Arg Met Ile Tyr Cys Glu Ser Ile Gly Asn Pro Ala Gly Asn Val Val
 145 150 155 160

Asp Ile Ala Ala Leu Ala Glu Val Ala His Ala Ala Gly Val Pro Leu
 165 170 175

Val Val Asp Asn Thr Val Pro Thr Pro Val Leu Cys Arg Pro Phe Glu
 180 185 190

His Gly Ala Asp Ile Val Val His Ala Leu Thr Lys Tyr Met Gly Gly
 195 200 205

His Gly Thr Ser Ile Gly Gly Ile Ile Val Asp Ser Gly Lys Phe Pro
 210 215 220

Trp Glu Gly Asn Ser Arg Phe Pro Gln Phe Asn Gln Pro Asp Pro Ser
 225 230 235 240

Tyr His Gly Val Val Tyr Val Asp Ala Phe Gly Pro Ala Ala Phe Ile
 245 250 255

Gly Arg Ala Arg Val Val Pro Leu Arg Asn Met Gly Ala Ala Ile Ser
 260 265 270

Pro Phe Asn Ser Phe Leu Ile Leu Gln Gly Ile Glu Thr Leu Pro Leu
 275 280 285

Arg Met Glu Arg His Cys Thr Asn Ala Leu Ala Ile Ala Arg Tyr Leu
 290 295 300

Gln Arg His Pro Lys Val Ser Trp Val Asn Phe Ala Gly Leu Glu Asp
 305 310 315 320

Asn Arg Asp Tyr Ala Leu Val Gln Lys Tyr Met Asp Gly Gly Ile Pro
 325 330 335

Ser Ser Ile Leu Ser Phe Gly Ile Lys Gly Gly Arg Glu Ala Cys Ala
 340 345 350

Arg Phe Met Asp Arg Leu Met Leu Ile Lys Arg Leu Val Asn Ile Gly
 355 360 365

Asp Ala Lys Thr Leu Ala Cys His Pro Ala Thr Thr Thr His Arg Gln
 370 375 380

Leu Asn Asp Glu Glu Leu Ala Lys Ala Gly Val Ser Ala Asp Leu Val
 385 390 395 400

Arg Leu Cys Val Gly Ile Glu His Ile Asp Asp Leu Ile Ala Asp Val
 405 410 415

Glu Gln Ala Phe Gln Asp
 420

<210> 27

<211> 1281

<212> DNA

<213> *Sinorhizobium meliloti*

<220>

<221> CDS

<222> (1) .. (1281)

<400> 27

atg aaa gcc gga ccc gga ttc agc acg ctt gca att cac gcc ggg gcc 48
 Met Lys Ala Gly Pro Gly Phe Ser Thr Leu Ala Ile His Ala Gly Ala
 1 5 10 15

cag ccc gat ccg acg acc ggt gcg cgg gcg acg ccg atc tat cag acg 96
 Gln Pro Asp Pro Thr Thr Gly Ala Arg Ala Thr Pro Ile Tyr Gln Thr
 20 25 30

acc agc ttc gtc ttc aac gac acg gat cat gcg gcc gca ctc ttc ggc 144
 Thr Ser Phe Val Phe Asn Asp Thr Asp His Ala Ala Ala Leu Phe Gly
 35 40 45

ctc	cag	caa	ttc	ggc	aat	atc	tat	acc	cgc	atc	atg	aat	ccg	acg	cag	192
Leu	Gln	Gln	Phe	Gly	Asn	Ile	Tyr	Thr	Arg	Ile	Met	Asn	Pro	Thr	Gln	
50						55					60					
gcg	gtg	ctg	gag	gag	cgg	atc	gcg	gcg	ctc	gaa	ggc	ggg	acc	gcc	ggg	240
Ala	Val	Leu	Glu	Glu	Arg	Ile	Ala	Ala	Leu	Glu	Gly	Gly	Thr	Ala	Gly	
65					70					75					80	
ctg	gcc	gtt	tcc	tcg	ggg	cat	gcg	gcc	cag	ctg	ctg	gtt	ttc	cat	acg	288
Leu	Ala	Val	Ser	Ser	Gly	His	Ala	Ala	Gln	Leu	Leu	Val	Phe	His	Thr	
			85						90					95		
atc	atg	agg	ccg	ggt	gac	aat	ttc	gtt	tcc	gcc	aga	cag	ctt	tac	ggc	336
Ile	Met	Arg	Pro	Gly	Asp	Asn	Phe	Val	Ser	Ala	Arg	Gln	Leu	Tyr	Gly	
			100					105					110			
ggg	tcg	gcc	aat	cag	ttc	ggc	cat	gcc	ttc	aag	gcc	ttc	gac	tgg	cag	384
Gly	Ser	Ala	Asn	Gln	Phe	Gly	His	Ala	Phe	Lys	Ala	Phe	Asp	Trp	Gln	
		115					120						125			
gtc	cgc	tgg	gcc	gat	tcg	gcg	gag	ccc	gaa	agc	ttc	gat	gcg	cag	atc	432
Val	Arg	Trp	Ala	Asp	Ser	Ala	Glu	Pro	Glu	Ser	Phe	Asp	Ala	Gln	Ile	
	130					135						140				
gac	gaa	cgc	acc	aag	gcg	atc	ttc	atc	gaa	agc	ctc	gcc	aat	ccg	ggc	480
Asp	Glu	Arg	Thr	Lys	Ala	Ile	Phe	Ile	Glu	Ser	Leu	Ala	Asn	Pro	Gly	
145					150					155					160	
ggc	acc	ttc	gtc	gac	ata	gcc	gca	atc	gct	gac	gtt	gcg	cgg	cga	cac	528
Gly	Thr	Phe	Val	Asp	Ile	Ala	Ala	Ile	Ala	Asp	Val	Ala	Arg	Arg	His	
				165					170					175		
gga	ctg	ccg	ctc	atc	gtc	gac	aat	acg	atg	gcg	acg	ccc	tat	ctg	atg	576
Gly	Leu	Pro	Leu	Ile	Val	Asp	Asn	Thr	Met	Ala	Thr	Pro	Tyr	Leu	Met	
			180					185					190			
cgg	ccg	ctc	gaa	cac	ggc	gcc	gat	atc	gtc	gtc	cat	tcg	ctc	acc	aag	624
Arg	Pro	Leu	Glu	His	Gly	Ala	Asp	Ile	Val	Val	His	Ser	Leu	Thr	Lys	
		195					200					205				
ttc	atc	ggc	ggt	cac	ggc	aat	tcg	atg	ggc	ggc	atc	atc	gtc	gac	ggc	672
Phe	Ile	Gly	Gly	His	Gly	Asn	Ser	Met	Gly	Gly	Ile	Ile	Val	Asp	Gly	
	210					215					220					
ggt	acg	ttc	gac	tgg	tcg	aaa	tcc	ggc	aag	tat	ccg	ctg	ctg	tcg	gag	720
Gly	Thr	Phe	Asp	Trp	Ser	Lys	Ser	Gly	Lys	Tyr	Pro	Leu	Leu	Ser	Glu	
225						230				235					240	
ccg	agg	ccc	gaa	tat	ggc	ggc	gtc	gtc	ctg	cac	cag	gcc	ttc	ggc	aac	768
Pro	Arg	Pro	Glu	Tyr	Gly	Gly	Val	Val	Leu	His	Gln	Ala	Phe	Gly	Asn	
				245					250					255		
ttc	gcc	ttc	gcc	atc	gcc	gca	cgg	gta	ttg	ggt	ctg	agg	gac	ttc	ggt	816
Phe	Ala	Phe	Ala	Ile	Ala	Ala	Arg	Val	Leu	Gly	Leu	Arg	Asp	Phe	Gly	
			260				265						270			
ccg	gcc	att	tcg	ccc	ttc	aac	gcc	ttc	ctg	atc	cag	acc	ggc	gtc	gag	864
Pro	Ala	Ile	Ser	Pro	Phe	Asn	Ala	Phe	Leu	Ile	Gln	Thr	Gly	Val	Glu	
		275					280						285			

acg ctg ccg ctg agg atg cag cgc cat tgc gac aac gcg ctg gag gtc 912
 Thr Leu Pro Leu Arg Met Gln Arg His Cys Asp Asn Ala Leu Glu Val
 290 295 300

gcc aaa tgg ctg aag gga cat gaa aag gtc tcc tgg gtc cgc tat tcc 960
 Ala Lys Trp Leu Lys Gly His Glu Lys Val Ser Trp Val Arg Tyr Ser
 305 310 315 320

ggg ctc gaa gac gat ccg aac cac gca ctg cag aaa cgc tac tcg ccg 1008
 Gly Leu Glu Asp Asp Pro Asn His Ala Leu Gln Lys Arg Tyr Ser Pro
 325 330 335

aag ggg gcg gga gcc gtt ttc acc ttc ggg ctc gcg ggc gga tac gag 1056
 Lys Gly Ala Gly Ala Val Phe Thr Phe Gly Leu Ala Gly Gly Tyr Glu
 340 345 350

gcg gga aag cgc ttt gtc gag gca ctg gaa atg ttc tcc cat ctt gcc 1104
 Ala Gly Lys Arg Phe Val Glu Ala Leu Glu Met Phe Ser His Leu Ala
 355 360 365

aat atc ggc gac acg cgt tcg ctc gtc atc cac ccc gca tcg acc acg 1152
 Asn Ile Gly Asp Thr Arg Ser Leu Val Ile His Pro Ala Ser Thr Thr
 370 375 380

cac cgg cag ctc acg ccg gag cag cag gtc gcc gca ggc gcc gga ccc 1200
 His Arg Gln Leu Thr Pro Glu Gln Gln Val Ala Ala Gly Ala Gly Pro
 385 390 395 400

gac gtc atc cgg ttg tcg gtc ggc atc gag gat gtg gcc gac atc att 1248
 Asp Val Ile Arg Leu Ser Val Gly Ile Glu Asp Val Ala Asp Ile Ile
 405 410 415

gcc gat ctc gaa cag gcg ctg ggc aag gcc tga 1281
 Ala Asp Leu Glu Gln Ala Leu Gly Lys Ala
 420 425

<210> 28

<211> 426

<212> PRT

<213> Sinorhizobium meliloti

<400> 28

Met Lys Ala Gly Pro Gly Phe Ser Thr Leu Ala Ile His Ala Gly Ala
 1 5 10 15

Gln Pro Asp Pro Thr Thr Gly Ala Arg Ala Thr Pro Ile Tyr Gln Thr
 20 25 30

Thr Ser Phe Val Phe Asn Asp Thr Asp His Ala Ala Ala Leu Phe Gly
 35 40 45

Leu Gln Gln Phe Gly Asn Ile Tyr Thr Arg Ile Met Asn Pro Thr Gln
 50 55 60

Ala Val Leu Glu Glu Arg Ile Ala Ala Leu Glu Gly Gly Thr Ala Gly
 65 70 75 80

Leu Ala Val Ser Ser Gly His Ala Ala Gln Leu Leu Val Phe His Thr
 85 90 95

Ile Met Arg Pro Gly Asp Asn Phe Val Ser Ala Arg Gln Leu Tyr Gly
 100 105 110

Gly Ser Ala Asn Gln Phe Gly His Ala Phe Lys Ala Phe Asp Trp Gln
 115 120 125

Val Arg Trp Ala Asp Ser Ala Glu Pro Glu Ser Phe Asp Ala Gln Ile
 130 135 140

Asp Glu Arg Thr Lys Ala Ile Phe Ile Glu Ser Leu Ala Asn Pro Gly
 145 150 155 160

Gly Thr Phe Val Asp Ile Ala Ala Ile Ala Asp Val Ala Arg Arg His
 165 170 175

Gly Leu Pro Leu Ile Val Asp Asn Thr Met Ala Thr Pro Tyr Leu Met
 180 185 190

Arg Pro Leu Glu His Gly Ala Asp Ile Val Val His Ser Leu Thr Lys
 195 200 205

Phe Ile Gly Gly His Gly Asn Ser Met Gly Gly Ile Ile Val Asp Gly
 210 215 220

Gly Thr Phe Asp Trp Ser Lys Ser Gly Lys Tyr Pro Leu Leu Ser Glu
 225 230 235 240

Pro Arg Pro Glu Tyr Gly Gly Val Val Leu His Gln Ala Phe Gly Asn
 245 250 255

Phe Ala Phe Ala Ile Ala Ala Arg Val Leu Gly Leu Arg Asp Phe Gly
 260 265 270

Pro Ala Ile Ser Pro Phe Asn Ala Phe Leu Ile Gln Thr Gly Val Glu
 275 280 285

Thr Leu Pro Leu Arg Met Gln Arg His Cys Asp Asn Ala Leu Glu Val
 290 295 300

Ala Lys Trp Leu Lys Gly His Glu Lys Val Ser Trp Val Arg Tyr Ser
 305 310 315 320

Gly Leu Glu Asp Asp Pro Asn His Ala Leu Gln Lys Arg Tyr Ser Pro
 325 330 335

Lys Gly Ala Gly Ala Val Phe Thr Phe Gly Leu Ala Gly Gly Tyr Glu
 340 345 350

Ala Gly Lys Arg Phe Val Glu Ala Leu Glu Met Phe Ser His Leu Ala
 355 360 365

Asn Ile Gly Asp Thr Arg Ser Leu Val Ile His Pro Ala Ser Thr Thr
 370 375 380

His Arg Gln Leu Thr Pro Glu Gln Gln Val Ala Ala Gly Ala Gly Pro
 385 390 395 400

Asp Val Ile Arg Leu Ser Val Gly Ile Glu Asp Val Ala Asp Ile Ile
 405 410 415

Ala Asp Leu Glu Gln Ala Leu Gly Lys Ala
 420 425

<210> 29

<211> 1293

<212> DNA

<213> Thermotoga maritima

<220>

<221> CDS

<222> (1)..(1293)

<400> 29

atg gac tgg aag aaa tac ggt tac aac aca agg gct ctt cac gca ggt
 Met Asp Trp Lys Lys Tyr Gly Tyr Asn Thr Arg Ala Leu His Ala Gly
 1 5 10 15

48

tat gaa cca ccc gag cag gcc aca gga tcg aga gcg gtc cct ata tat	96
Tyr Glu Pro Pro Glu Gln Ala Thr Gly Ser Arg Ala Val Pro Ile Tyr	
20 25 30	
caa acg act tct tac gtt ttc aga gac tct gat cac gcg gcg aga ctc	144
Gln Thr Thr Ser Tyr Val Phe Arg Asp Ser Asp His Ala Ala Arg Leu	
35 40 45	
ttc gca ctg gaa gaa cct ggg ttc atc tat aca agg att gga aat cct	192
Phe Ala Leu Glu Glu Pro Gly Phe Ile Tyr Thr Arg Ile Gly Asn Pro	
50 55 60	
acc gtc tca gtt ctt gaa gaa aga ata gcc gcc ctg gaa gaa ggg gtg	240
Thr Val Ser Val Leu Glu Glu Arg Ile Ala Ala Leu Glu Glu Gly Val	
65 70 75 80	
gga gcc tta gcg gtt gcc agt gga caa gcc gct ata act tac gcc att	288
Gly Ala Leu Ala Val Ala Ser Gly Gln Ala Ala Ile Thr Tyr Ala Ile	
85 90 95	
ttg aac atc gcg ggc cca gga gat gag atc gtc agc ggg agc gcg ctg	336
Leu Asn Ile Ala Gly Pro Gly Asp Glu Ile Val Ser Gly Ser Ala Leu	
100 105 110	
tat ggg gga acg tac aat ctg ttc aga cac act ctc tat aaa aaa tcc	384
Tyr Gly Gly Thr Tyr Asn Leu Phe Arg His Thr Leu Tyr Lys Lys Ser	
115 120 125	
ggc atc atc gtg aag ttt gtg gat gag aca gat cca aag aac ata gaa	432
Gly Ile Ile Val Lys Phe Val Asp Glu Thr Asp Pro Lys Asn Ile Glu	
130 135 140	
gag gcc atc acc gag aaa aca aag gcg gtg tac ctt gaa act atc ggg	480
Glu Ala Ile Thr Glu Lys Thr Lys Ala Val Tyr Leu Glu Thr Ile Gly	
145 150 155 160	
aat ccc ggt ctc aca gtg ccg gac ttt gaa gcg ata gcg gag atc gct	528
Asn Pro Gly Leu Thr Val Pro Asp Phe Glu Ala Ile Ala Glu Ile Ala	
165 170 175	
cac aga cac ggt gtt cct ttg ata gtg gac aat acg gta gct ccg tac	576
His Arg His Gly Val Pro Leu Ile Val Asp Asn Thr Val Ala Pro Tyr	
180 185 190	
ata ttc agg ccc ttc gaa cac ggt gcc gac atc gtt gtt tat tcg gcc	624
Ile Phe Arg Pro Phe Glu His Gly Ala Asp Ile Val Val Tyr Ser Ala	
195 200 205	
acg aaa ttc atc gga gga cac gga aca tcg ata ggc ggt ctc atc gta	672
Thr Lys Phe Ile Gly Gly His Gly Thr Ser Ile Gly Gly Leu Ile Val	
210 215 220	
gac agc gga aaa ttc gac tgg acg aac gga aag ttt cca gaa ctc gtg	720
Asp Ser Gly Lys Phe Asp Trp Thr Asn Gly Lys Phe Pro Glu Leu Val	
225 230 235 240	
gaa cca gat ccc agc tac cac ggt gtg agt tat gtg gag acg ttc aaa	768
Glu Pro Asp Pro Ser Tyr His Gly Val Ser Tyr Val Glu Thr Phe Lys	
245 250 255	

gaa gca gcc tac ata gca aaa tgt aga acc cag ctt ttg agg gac ctg 816
 Glu Ala Ala Tyr Ile Ala Lys Cys Arg Thr Gln Leu Leu Arg Asp Leu
 260 265 270

gga agc tgt atg agc ccg ttc aac gcg ttt ctg ttc atc ctc gga ctt 864
 Gly Ser Cys Met Ser Pro Phe Asn Ala Phe Leu Phe Ile Leu Gly Leu
 275 280 285

gaa acc ctc agc ttg agg atg aag aaa cac tgt gaa aac gca ctg aag 912
 Glu Thr Leu Ser Leu Arg Met Lys Lys His Cys Glu Asn Ala Leu Lys
 290 295 300

atc gtt gaa ttt ctg aaa tcg cat ccc gcc gtg agc tgg gtc aac tat 960
 Ile Val Glu Phe Leu Lys Ser His Pro Ala Val Ser Trp Val Asn Tyr
 305 310 315 320

ccg ata gct gaa ggc aat aaa acc aga gaa aat gcg ctg aaa tac ctc 1008
 Pro Ile Ala Glu Gly Asn Lys Thr Arg Glu Asn Ala Leu Lys Tyr Leu
 325 330 335

aaa gaa gga tac ggt gcg att gta acg ttc ggt gtg aaa ggc gga aaa 1056
 Lys Glu Gly Tyr Gly Ala Ile Val Thr Phe Gly Val Lys Gly Gly Lys
 340 345 350

gag gcg gga aag aag ttc ata gac agt ctc aca ctc att tcc cac ctc 1104
 Glu Ala Gly Lys Lys Phe Ile Asp Ser Leu Thr Leu Ile Ser His Leu
 355 360 365

gcc aac att ggt gat gca aga act ctg gct att cat ccc gct tcg aca 1152
 Ala Asn Ile Gly Asp Ala Arg Thr Leu Ala Ile His Pro Ala Ser Thr
 370 375 380

acc cat cag cag ctc acg gaa gaa gag cag ttg aaa acg ggt gtt act 1200
 Thr His Gln Gln Leu Thr Glu Glu Glu Gln Leu Lys Thr Gly Val Thr
 385 390 395 400

ccg gat atg ata aga ttg tct gtt gga ata gaa gat gtg gaa gat atc 1248
 Pro Asp Met Ile Arg Leu Ser Val Gly Ile Glu Asp Val Glu Asp Ile
 405 410 415

ata gcc gat ctg gat cag gct ctc aga aaa tct cag gag gga tga 1293
 Ile Ala Asp Leu Asp Gln Ala Leu Arg Lys Ser Gln Glu Gly
 420 425 430

<210> 30

<211> 430

<212> PRT

<213> Thermotoga maritima

<400> 30

Met Asp Trp Lys Lys Tyr Gly Tyr Asn Thr Arg Ala Leu His Ala Gly
 1 5 10 15

Tyr Glu Pro Pro Glu Gln Ala Thr Gly Ser Arg Ala Val Pro Ile Tyr
 20 25 30

Gln Thr Thr Ser Tyr Val Phe Arg Asp Ser Asp His Ala Ala Arg Leu
 35 40 45

Phe Ala Leu Glu Glu Pro Gly Phe Ile Tyr Thr Arg Ile Gly Asn Pro
 50 55 60

Thr Val Ser Val Leu Glu Glu Arg Ile Ala Ala Leu Glu Glu Gly Val
 65 70 75 80

Gly Ala Leu Ala Val Ala Ser Gly Gln Ala Ala Ile Thr Tyr Ala Ile
 85 90 95

Leu Asn Ile Ala Gly Pro Gly Asp Glu Ile Val Ser Gly Ser Ala Leu
 100 105 110

Tyr Gly Gly Thr Tyr Asn Leu Phe Arg His Thr Leu Tyr Lys Lys Ser
 115 120 125

Gly Ile Ile Val Lys Phe Val Asp Glu Thr Asp Pro Lys Asn Ile Glu
 130 135 140

Glu Ala Ile Thr Glu Lys Thr Lys Ala Val Tyr Leu Glu Thr Ile Gly
 145 150 155 160

Asn Pro Gly Leu Thr Val Pro Asp Phe Glu Ala Ile Ala Glu Ile Ala
 165 170 175

His Arg His Gly Val Pro Leu Ile Val Asp Asn Thr Val Ala Pro Tyr
 180 185 190

Ile Phe Arg Pro Phe Glu His Gly Ala Asp Ile Val Val Tyr Ser Ala
 195 200 205

Thr Lys Phe Ile Gly Gly His Gly Thr Ser Ile Gly Gly Leu Ile Val
 210 215 220

Asp Ser Gly Lys Phe Asp Trp Thr Asn Gly Lys Phe Pro Glu Leu Val
 225 230 235 240

Glu Pro Asp Pro Ser Tyr His Gly Val Ser Tyr Val Glu Thr Phe Lys

245

250

255

Glu Ala Ala Tyr Ile Ala Lys Cys Arg Thr Gln Leu Leu Arg Asp Leu
 260 265 270

Gly Ser Cys Met Ser Pro Phe Asn Ala Phe Leu Phe Ile Leu Gly Leu
 275 280 285

Glu Thr Leu Ser Leu Arg Met Lys Lys His Cys Glu Asn Ala Leu Lys
 290 295 300

Ile Val Glu Phe Leu Lys Ser His Pro Ala Val Ser Trp Val Asn Tyr
 305 310 315 320

Pro Ile Ala Glu Gly Asn Lys Thr Arg Glu Asn Ala Leu Lys Tyr Leu
 325 330 335

Lys Glu Gly Tyr Gly Ala Ile Val Thr Phe Gly Val Lys Gly Gly Lys
 340 345 350

Glu Ala Gly Lys Lys Phe Ile Asp Ser Leu Thr Leu Ile Ser His Leu
 355 360 365

Ala Asn Ile Gly Asp Ala Arg Thr Leu Ala Ile His Pro Ala Ser Thr
 370 375 380

Thr His Gln Gln Leu Thr Glu Glu Glu Gln Leu Lys Thr Gly Val Thr
 385 390 395 400

Pro Asp Met Ile Arg Leu Ser Val Gly Ile Glu Asp Val Glu Asp Ile
 405 410 415

Ile Ala Asp Leu Asp Gln Ala Leu Arg Lys Ser Gln Glu Gly
 420 425 430

<210> 31

<211> 1314

<212> DNA

<213> Streptococcus mutans

<220>

<221> CDS

<222> (1)..(1314)

<400> 31

atg gag cta att aat aat aaa agg aga gct tcc atg act cga gaa ttt	48
Met Glu Leu Ile Asn Asn Lys Arg Arg Ala Ser Met Thr Arg Glu Phe	
1 5 10 15	
tct ttt gaa act tta caa tta cat gcg gga caa agt gtt gat cct aca	96
Ser Phe Glu Thr Leu Gln Leu His Ala Gly Gln Ser Val Asp Pro Thr	
20 25 30	
aca aaa tcg cgt gca gta cca atc tat cag acg act tcc tat gtg ttt	144
Thr Lys Ser Arg Ala Val Pro Ile Tyr Gln Thr Thr Ser Tyr Val Phe	
35 40 45	
aat gat gca caa gat gct gaa gat tct ttt gca ctt cgt aca ccc ggc	192
Asn Asp Ala Gln Asp Ala Glu Asp Ser Phe Ala Leu Arg Thr Pro Gly	
50 55 60	
aat att tat acg cgg atc act aat ccg act aca gcc gtt ttt gaa gaa	240
Asn Ile Tyr Thr Arg Ile Thr Asn Pro Thr Thr Ala Val Phe Glu Glu	
65 70 75 80	
cgg atg gcc gct ctt gaa ggt ggt gtc ggt gca ctg gca aca gct tct	288
Arg Met Ala Ala Leu Glu Gly Gly Val Gly Ala Leu Ala Thr Ala Ser	
85 90 95	
ggt atg gca gca gta act tat att gcc ttg gct ctt gct cat gca ggt	336
Gly Met Ala Ala Val Thr Tyr Ile Ala Leu Ala Leu Ala His Ala Gly	
100 105 110	
gat cat att gtg tca gca gcg aca gtt tac ggt ggc act ttt aat ctt	384
Asp His Ile Val Ser Ala Ala Thr Val Tyr Gly Gly Thr Phe Asn Leu	
115 120 125	
ctt aag gaa act tta cct cgc tat ggc att act aca agt ttt gtt gat	432
Leu Lys Glu Thr Leu Pro Arg Tyr Gly Ile Thr Thr Ser Phe Val Asp	
130 135 140	
gtt gct aat ttc gct gaa att gaa gcg gct att aca gac aag act aag	480
Val Ala Asn Phe Ala Glu Ile Glu Ala Ala Ile Thr Asp Lys Thr Lys	
145 150 155 160	
ttt att atc gct gaa acg tta gga aat cct ctt gga aat atc gct gat	528
Phe Ile Ile Ala Glu Thr Leu Gly Asn Pro Leu Gly Asn Ile Ala Asp	
165 170 175	
ctt gaa aaa tta gct gag att gcc cat cga cat gct att ccc ttg gtt	576
Leu Glu Lys Leu Ala Glu Ile Ala His Arg His Ala Ile Pro Leu Val	
180 185 190	
att gat aat acc ttt ggt act cct tat ttg ctt aat gtc ttc tct tac	624
Ile Asp Asn Thr Phe Gly Thr Pro Tyr Leu Leu Asn Val Phe Ser Tyr	
195 200 205	
ggt gtt gat att gct gtt cat tct gcc act aaa ttt atc ggt gga cat	672

Gly Val Asp Ile Ala Val His Ser Ala Thr Lys Phe Ile Gly Gly His 210 215 220	
ggg aca tct att ggc ggt gtc att gtt gat tct gga aac ttt gat tgg Gly Thr Ser Ile Gly Gly Val Ile Val Asp Ser Gly Asn Phe Asp Trp 225 230 235 240	720
gaa aaa tct gga aaa ttc cca caa ttt gta gaa cca gat cct tcc tat Glu Lys Ser Gly Lys Phe Pro Gln Phe Val Glu Pro Asp Pro Ser Tyr 245 250 255	768
cat gac att agt tat aca cgt gat att gga aaa gca gct ttt gta act His Asp Ile Ser Tyr Thr Arg Asp Ile Gly Lys Ala Ala Phe Val Thr 260 265 270	816
gcg gtg cgt acg caa ctg ctg cgt gat aca ggc gcc tgc ctt tca cct Ala Val Arg Thr Gln Leu Leu Arg Asp Thr Gly Ala Cys Leu Ser Pro 275 280 285	864
ttc aat gcc ttt ctt ttg cta caa ggt cta gaa acc tta tca ctt cgt Phe Asn Ala Phe Leu Leu Leu Gln Gly Leu Glu Thr Leu Ser Leu Arg 290 295 300	912
gtt gag cgt cat gtg gaa aat gct aag aaa att gcg tac tat ctg gaa Val Glu Arg His Val Glu Asn Ala Lys Lys Ile Ala Tyr Tyr Leu Glu 305 310 315 320	960
aat cat cct aaa gtc aca aaa gtt aat tat gct agt ttg cca tca agt Asn His Pro Lys Val Thr Lys Val Asn Tyr Ala Ser Leu Pro Ser Ser 325 330 335	1008
cct tat tat gac ttg gct caa aaa tac ttg cca aaa gga gct agt tct Pro Tyr Tyr Asp Leu Ala Gln Lys Tyr Leu Pro Lys Gly Ala Ser Ser 340 345 350	1056
atc ttt act ttt aat gtt gca ggc agt gcg aaa gcc gct cgc gag gtc Ile Phe Thr Phe Asn Val Ala Gly Ser Ala Lys Ala Ala Arg Glu Val 355 360 365	1104
att gac agt ctt gaa atc ttt tct gat ttg gcg aat gtt gct gat gcc Ile Asp Ser Leu Glu Ile Phe Ser Asp Leu Ala Asn Val Ala Asp Ala 370 375 380	1152
aaa tca cta gtt gtt cat ccg gca aca acc act cat ggt caa atg act Lys Ser Leu Val Val His Pro Ala Thr Thr His Gly Gln Met Thr 385 390 395 400	1200
gaa gaa gat cta cga gct tgc ggt att gaa cct gag caa atc cgt gtt Glu Glu Asp Leu Arg Ala Cys Gly Ile Glu Pro Glu Gln Ile Arg Val 405 410 415	1248
tct att ggt ttg gaa aat gct gat gac tta atc gaa gat ttg cgc cta Ser Ile Gly Leu Glu Asn Ala Asp Asp Leu Ile Glu Asp Leu Arg Leu 420 425 430	1296
gca ctt gaa aaa ata taa Ala Leu Glu Lys Ile 435	1314

<210> 32

<211> 437

<212> PRT

<213> Streptococcus mutans

<400> 32

Met Glu Leu Ile Asn Asn Lys Arg Arg Ala Ser Met Thr Arg Glu Phe
1 5 10 15

Ser Phe Glu Thr Leu Gln Leu His Ala Gly Gln Ser Val Asp Pro Thr
20 25 30

Thr Lys Ser Arg Ala Val Pro Ile Tyr Gln Thr Thr Ser Tyr Val Phe
35 40 45

Asn Asp Ala Gln Asp Ala Glu Asp Ser Phe Ala Leu Arg Thr Pro Gly
50 55 60

Asn Ile Tyr Thr Arg Ile Thr Asn Pro Thr Thr Ala Val Phe Glu Glu
65 70 75 80

Arg Met Ala Ala Leu Glu Gly Gly Val Gly Ala Leu Ala Thr Ala Ser
85 90 95

Gly Met Ala Ala Val Thr Tyr Ile Ala Leu Ala Leu Ala His Ala Gly
100 105 110

Asp His Ile Val Ser Ala Ala Thr Val Tyr Gly Gly Thr Phe Asn Leu
115 120 125

Leu Lys Glu Thr Leu Pro Arg Tyr Gly Ile Thr Thr Ser Phe Val Asp
130 135 140

Val Ala Asn Phe Ala Glu Ile Glu Ala Ala Ile Thr Asp Lys Thr Lys
145 150 155 160

Phe Ile Ile Ala Glu Thr Leu Gly Asn Pro Leu Gly Asn Ile Ala Asp
165 170 175

Leu Glu Lys Leu Ala Glu Ile Ala His Arg His Ala Ile Pro Leu Val
180 185 190

Ile Asp Asn Thr Phe Gly Thr Pro Tyr Leu Leu Asn Val Phe Ser Tyr
 195 200 205

Gly Val Asp Ile Ala Val His Ser Ala Thr Lys Phe Ile Gly Gly His
 210 215 220

Gly Thr Ser Ile Gly Gly Val Ile Val Asp Ser Gly Asn Phe Asp Trp
 225 230 235 240

Glu Lys Ser Gly Lys Phe Pro Gln Phe Val Glu Pro Asp Pro Ser Tyr
 245 250 255

His Asp Ile Ser Tyr Thr Arg Asp Ile Gly Lys Ala Ala Phe Val Thr
 260 265 270

Ala Val Arg Thr Gln Leu Leu Arg Asp Thr Gly Ala Cys Leu Ser Pro
 275 280 285

Phe Asn Ala Phe Leu Leu Leu Gln Gly Leu Glu Thr Leu Ser Leu Arg
 290 295 300

Val Glu Arg His Val Glu Asn Ala Lys Lys Ile Ala Tyr Tyr Leu Glu
 305 310 315 320

Asn His Pro Lys Val Thr Lys Val Asn Tyr Ala Ser Leu Pro Ser Ser
 325 330 335

Pro Tyr Tyr Asp Leu Ala Gln Lys Tyr Leu Pro Lys Gly Ala Ser Ser
 340 345 350

Ile Phe Thr Phe Asn Val Ala Gly Ser Ala Lys Ala Ala Arg Glu Val
 355 360 365

Ile Asp Ser Leu Glu Ile Phe Ser Asp Leu Ala Asn Val Ala Asp Ala
 370 375 380

Lys Ser Leu Val Val His Pro Ala Thr Thr Thr His Gly Gln Met Thr
 385 390 395 400

Glu Glu Asp Leu Arg Ala Cys Gly Ile Glu Pro Glu Gln Ile Arg Val
 405 410 415

Ser Ile Gly Leu Glu Asn Ala Asp Asp Leu Ile Glu Asp Leu Arg Leu
 420 425 430

Ala Leu Glu Lys Ile
435

<210> 33

<211> 1431

<212> DNA

<213> Burkholderia cepacia

<220>

<221> CDS

<222> (1) .. (1431)

<400> 33

ttg aag cgc cgc acg ccg gtg ata gga tgg ccg cca ctt tca cct ttc	48
Leu Lys Arg Arg Thr Pro Val Ile Gly Trp Pro Pro Leu Ser Pro Phe	
1 5 10 15	
gcg agg ccg tcc gtg gcc ccg ccg ccc agc atg tcc gcg aac cgt ttc	96
Ala Arg Pro Ser Val Ala Pro Pro Pro Ser Met Ser Ala Asn Arg Phe	
20 25 30	
gac acg ctt gcg ctg cac gcc ggc gct gct ccc gac ccg acc acc ggc	144
Asp Thr Leu Ala Leu His Ala Gly Ala Ala Pro Asp Pro Thr Thr Gly	
35 40 45	
gcg cgc gcc acg ccg att tac cag act acc tcg ttt tcg ttc cgc gat	192
Ala Arg Ala Thr Pro Ile Tyr Gln Thr Thr Ser Phe Ser Phe Arg Asp	
50 55 60	
tcc gac cac gcc gcg gcg ctc ttc aat atg gag cgc gcc ggt cat gtt	240
Ser Asp His Ala Ala Ala Leu Phe Asn Met Glu Arg Ala Gly His Val	
65 70 75 80	
tat tcg cgc att tcg aac ccg acc gtg gcc gtg ttc gag gaa cgc gtg	288
Tyr Ser Arg Ile Ser Asn Pro Thr Val Ala Val Phe Glu Glu Arg Val	
85 90 95	
gcc gcg ctg gaa aac ggc gcg ggc gcg atc ggc acg gca agc ggc cag	336
Ala Ala Leu Glu Asn Gly Ala Gly Ala Ile Gly Thr Ala Ser Gly Gln	
100 105 110	
gcg gcc ctg cat ctg gcc att gcc acg ctg atg ggc gcg ggt tcg cat	384
Ala Ala Leu His Leu Ala Ile Ala Thr Leu Met Gly Ala Gly Ser His	
115 120 125	
atc gtc gcc tcc agc gcg ctg tac ggc ggc tcg cac aat ctg ctg cac	432
Ile Val Ala Ser Ser Ala Leu Tyr Gly Gly Ser His Asn Leu Leu His	
130 135 140	

tac acg ttg cgg cgc ttc ggc atc gag acg act ttc gtc aaa ccc ggc Tyr Thr Leu Arg Arg Phe Gly Ile Glu Thr Thr Phe Val Lys Pro Gly 145 150 155 160	480
gac ctg gac gcg tgg cgc gcc gcg ctg cgc cca aac acg cgg ctg ctg Asp Leu Asp Ala Trp Arg Ala Ala Leu Arg Pro Asn Thr Arg Leu Leu 165 170 175	528
ttc ggc gag acg ctc ggc aat ccg ggg ctc gac gtg ctc gat atc gcc Phe Gly Glu Thr Leu Gly Asn Pro Gly Leu Asp Val Leu Asp Ile Ala 180 185 190	576
gcc gtc gcg cag atc gcg cat gag cac cgc gtg ccg ctg ctg gtc gac Ala Val Ala Gln Ile Ala His Glu His Arg Val Pro Leu Leu Val Asp 195 200 205	624
tcg acc ttc acc aca cct tac ctg ctc aaa ccg ttc gaa cat ggc gcg Ser Thr Phe Thr Thr Pro Tyr Leu Leu Lys Pro Phe Glu His Gly Ala 210 215 220	672
gac ttc gtc tat cac tcg gcc acc aaa ttc ctc ggc ggc cac ggc acg Asp Phe Val Tyr His Ser Ala Thr Lys Phe Leu Gly Gly His Gly Thr 225 230 235 240	720
acg atc ggc ggc gtg ctg gtg gac ggc ggc acg ttc gac ttc gac gcc Thr Ile Gly Gly Val Leu Val Asp Gly Gly Thr Phe Asp Phe Asp Ala 245 250 255	768
tcg ggg cgc ttc ccc gaa ttc acc gaa cct tac gac ggc ttt cac ggc Ser Gly Arg Phe Pro Glu Phe Thr Glu Pro Tyr Asp Gly Phe His Gly 260 265 270	816
atg gtg ttc gcc gag gag agc acc gtc gcg ccg ttt ctg ctg cga gca Met Val Phe Ala Glu Glu Ser Thr Val Ala Pro Phe Leu Leu Arg Ala 275 280 285	864
cgc cgc gag ggg ctg cgc gac ttc ggc gca tgc ctg cat ccg caa gcc Arg Arg Glu Gly Leu Arg Asp Phe Gly Ala Cys Leu His Pro Gln Ala 290 295 300	912
gca tgg caa ctg ctg caa ggc atc gag acg ctg ccg ttg cga atg gaa Ala Trp Gln Leu Leu Gln Gly Ile Glu Thr Leu Pro Leu Arg Met Glu 305 310 315 320	960
cgg cac gtt gcc aac acg cgc cgg gtg gtc gag ttc ctc gcc ggt cac Arg His Val Ala Asn Thr Arg Arg Val Val Glu Phe Leu Ala Gly His 325 330 335	1008
gcc gcg gtc ggg gcc gtc gcc tat ccg gaa ctg ccc acg cac ccc gac Ala Ala Val Gly Ala Val Ala Tyr Pro Glu Leu Pro Thr His Pro Asp 340 345 350	1056
cac gcg ctc gcg aag cgg ctg ctg ccg cgc ggc gcc ggt gcc gtg ttc His Ala Leu Ala Lys Arg Leu Leu Pro Arg Gly Ala Gly Ala Val Phe 355 360 365	1104
agc ttc gat ctg cgc ggc gac cgc gcc gcc gga cgc agc ttt atc gaa Ser Phe Asp Leu Arg Gly Asp Arg Ala Ala Gly Arg Ser Phe Ile Glu 370 375 380	1152

gcg ctc tcg ctg ttc tcg cat ctc gcg aac gtg ggc gac gcg cgc tcg 1200
 Ala Leu Ser Leu Phe Ser His Leu Ala Asn Val Gly Asp Ala Arg Ser
 385 390 395 400

ctc gtg atc cat ccc gcc tcg acc acc cac ttt cgc atg gac gcc gct 1248
 Leu Val Ile His Pro Ala Ser Thr Thr His Phe Arg Met Asp Ala Ala
 405 410 415

gcc ctt gcc gcg gcc ggt atc gcc gaa ggc acg atc cgc ctc tcg atc 1296
 Ala Leu Ala Ala Ala Gly Ile Ala Glu Gly Thr Ile Arg Leu Ser Ile
 420 425 430

ggc ctc gaa gat ccc gac gat ctg atc gac gat ctc aag cgc gcg cta 1344
 Gly Leu Glu Asp Pro Asp Asp Leu Ile Asp Asp Leu Lys Arg Ala Leu
 435 440 445

aag gcc gca cag aaa gcg ggc agt tcg agc gca gcg cac ggc ggc gca 1392
 Lys Ala Ala Gln Lys Ala Gly Ser Ser Ser Ala Ala His Gly Gly Ala
 450 455 460

tcc ggc agt gcc gcc caa ccc cgc ccg gag tcc gca tga 1431
 Ser Gly Ser Ala Ala Gln Pro Arg Pro Glu Ser Ala
 465 470 475

<210> 34

<211> 476

<212> PRT

<213> Burkholderia cepacia

<400> 34

Leu Lys Arg Arg Thr Pro Val Ile Gly Trp Pro Pro Leu Ser Pro Phe
 1 5 10 15

Ala Arg Pro Ser Val Ala Pro Pro Pro Ser Met Ser Ala Asn Arg Phe
 20 25 30

Asp Thr Leu Ala Leu His Ala Gly Ala Ala Pro Asp Pro Thr Thr Gly
 35 40 45

Ala Arg Ala Thr Pro Ile Tyr Gln Thr Thr Ser Phe Ser Phe Arg Asp
 50 55 60

Ser Asp His Ala Ala Ala Leu Phe Asn Met Glu Arg Ala Gly His Val
 65 70 75 80

Tyr Ser Arg Ile Ser Asn Pro Thr Val Ala Val Phe Glu Glu Arg Val
 85 90 95

Ala Ala Leu Glu Asn Gly Ala Gly Ala Ile Gly Thr Ala Ser Gly Gln
 100 105 110

Ala Ala Leu His Leu Ala Ile Ala Thr Leu Met Gly Ala Gly Ser His
 115 120 125

Ile Val Ala Ser Ser Ala Leu Tyr Gly Gly Ser His Asn Leu Leu His
 130 135 140

Tyr Thr Leu Arg Arg Phe Gly Ile Glu Thr Thr Phe Val Lys Pro Gly
 145 150 155 160

Asp Leu Asp Ala Trp Arg Ala Ala Leu Arg Pro Asn Thr Arg Leu Leu
 165 170 175

Phe Gly Glu Thr Leu Gly Asn Pro Gly Leu Asp Val Leu Asp Ile Ala
 180 185 190

Ala Val Ala Gln Ile Ala His Glu His Arg Val Pro Leu Leu Val Asp
 195 200 205

Ser Thr Phe Thr Thr Pro Tyr Leu Leu Lys Pro Phe Glu His Gly Ala
 210 215 220

Asp Phe Val Tyr His Ser Ala Thr Lys Phe Leu Gly Gly His Gly Thr
 225 230 235 240

Thr Ile Gly Gly Val Leu Val Asp Gly Gly Thr Phe Asp Phe Asp Ala
 245 250 255

Ser Gly Arg Phe Pro Glu Phe Thr Glu Pro Tyr Asp Gly Phe His Gly
 260 265 270

Met Val Phe Ala Glu Glu Ser Thr Val Ala Pro Phe Leu Leu Arg Ala
 275 280 285

Arg Arg Glu Gly Leu Arg Asp Phe Gly Ala Cys Leu His Pro Gln Ala
 290 295 300

Ala Trp Gln Leu Leu Gln Gly Ile Glu Thr Leu Pro Leu Arg Met Glu
 305 310 315 320

Arg His Val Ala Asn Thr Arg Arg Val Val Glu Phe Leu Ala Gly His
 325 330 335

Ala Ala Val Gly Ala Val Ala Tyr Pro Glu Leu Pro Thr His Pro Asp
 340 345 350

His Ala Leu Ala Lys Arg Leu Leu Pro Arg Gly Ala Gly Ala Val Phe
 355 360 365

Ser Phe Asp Leu Arg Gly Asp Arg Ala Ala Gly Arg Ser Phe Ile Glu
 370 375 380

Ala Leu Ser Leu Phe Ser His Leu Ala Asn Val Gly Asp Ala Arg Ser
 385 390 395 400

Leu Val Ile His Pro Ala Ser Thr Thr His Phe Arg Met Asp Ala Ala
 405 410 415

Ala Leu Ala Ala Ala Gly Ile Ala Glu Gly Thr Ile Arg Leu Ser Ile
 420 425 430

Gly Leu Glu Asp Pro Asp Asp Leu Ile Asp Asp Leu Lys Arg Ala Leu
 435 440 445

Lys Ala Ala Gln Lys Ala Gly Ser Ser Ser Ala Ala His Gly Gly Ala
 450 455 460

Ser Gly Ser Ala Ala Gln Pro Arg Pro Glu Ser Ala
 465 470 475

<210> 35

<211> 1722

<212> DNA

<213> *Deinococcus radiodurans*

<220>

<221> CDS

<222> (1)..(1722)

<400> 35

gtg gcc ttc ccg tgc ggt cag gcg ggg aac aag ata aca agg ccg ggc
 Val Ala Phe Pro Cys Gly Gln Ala Gly Asn Lys Ile Thr Arg Pro Gly
 1 5 10 15

48

caa tgt gtc aac ggg ggc agg gca cgc tca gcc ccg tct aag ttt cgc	96
Gln Cys Val Asn Gly Gly Arg Ala Arg Ser Ala Pro Ser Lys Phe Arg	
20 25 30	
ctt gac ccc tta ccc gcc tcc gcg cta ctt ttt gag gag ctc ccg cag	144
Leu Asp Pro Leu Pro Ala Ser Ala Leu Leu Phe Glu Glu Leu Pro Gln	
35 40 45	
cag gag cca ccc act tca gag cgc ccg aga gac ctg gct cga cga cgg	192
Gln Glu Pro Pro Thr Ser Glu Arg Pro Arg Asp Leu Ala Arg Arg Arg	
50 55 60	
cgc ggc aac cgg acc cca tca cgt cac ggt gcc aag gcc agc ccc ctg	240
Arg Gly Asn Arg Thr Pro Ser Arg His Gly Ala Lys Ala Ser Pro Leu	
65 70 75 80	
ggc gtg tca acg atg agc cgc cgg gcg gga cca agc ggg aag gcc acg	288
Gly Val Ser Thr Met Ser Arg Arg Ala Gly Pro Ser Gly Lys Ala Thr	
85 90 95	
cgg atg acg ata ttc aag tgt ccc ttc tcg att cac agc agg cag ggg	336
Arg Met Thr Ile Phe Lys Cys Pro Phe Ser Ile His Ser Arg Gln Gly	
100 105 110	
gag tgc cgt gac tgg cgc ccc cga acc tgc ttc ccc cga gga gcc gcc	384
Glu Cys Arg Asp Trp Arg Pro Arg Thr Cys Phe Pro Arg Gly Ala Ala	
115 120 125	
acc atg acc gat acc aaa cag ccg cag cct ctg cac ttc gag acc ttg	432
Thr Met Thr Asp Thr Lys Gln Pro Gln Pro Leu His Phe Glu Thr Leu	
130 135 140	
cag gtg cac gcc gga caa cgc ccc gac ccc gtg acc gga gcg cag caa	480
Gln Val His Ala Gly Gln Arg Pro Asp Pro Val Thr Gly Ala Gln Gln	
145 150 155 160	
acg ccc atc tac gcc acc aac tcc tac gtg ttc gag tcg ccc gag cac	528
Thr Pro Ile Tyr Ala Thr Asn Ser Tyr Val Phe Glu Ser Pro Glu His	
165 170 175	
gcc gcc gac ctc ttc ggg ctg cgg caa ttc ggc aac atc tac agc cgc	576
Ala Ala Asp Leu Phe Gly Leu Arg Gln Phe Gly Asn Ile Tyr Ser Arg	
180 185 190	
atc atg aac ccc acc aac gac gtg ttc gag cag cgg gtg gcc gcc ctc	624
Ile Met Asn Pro Thr Asn Asp Val Phe Glu Gln Arg Val Ala Ala Leu	
195 200 205	
gaa ggg ggc gtg ggg gcg ctg tcg gtg tcg agc ggg cac gcg ggg cag	672
Glu Gly Gly Val Gly Ala Leu Ser Val Ser Ser Gly His Ala Gly Gln	
210 215 220	
ctc gtg aca ttg ctc acg ctg gcg cag gcg gga gac aac atc gtc tcg	720
Leu Val Thr Leu Leu Thr Leu Ala Gln Ala Gly Asp Asn Ile Val Ser	
225 230 235 240	
tcg ccc aac ctg tac ggc ggc acc gtc aac cag ttc cgc gtc acg ctc	768
Ser Pro Asn Leu Tyr Gly Gly Thr Val Asn Gln Phe Arg Val Thr Leu	
245 250 255	

aag cgg ctc ggc atc gag gtg cgg ttt acc agc aaa gac gag cgc ccc Lys Arg Leu Gly Ile Glu Val Arg Phe Thr Ser Lys Asp Glu Arg Pro 260 265 270	816
gag gaa ttc gcc gcg ctg atc gac gag cgc acg cgg gcc gta tat ctg Glu Glu Phe Ala Ala Leu Ile Asp Glu Arg Thr Arg Ala Val Tyr Leu 275 280 285	864
gaa acc atc ggc aac ccg gcg ctg aac att ccc gat ttc gag ggc gtg Glu Thr Ile Gly Asn Pro Ala Leu Asn Ile Pro Asp Phe Glu Gly Val 290 295 300	912
gcg aaa gtc gcg cac gag cac ggc gtc gcg gtg gtc gtg gac aac acc Ala Lys Val Ala His Glu His Gly Val Ala Val Val Val Asp Asn Thr 305 310 315 320	960
ttc ggg gcc ggc gga tac tac tgc cag ccg ctg cgg cac ggc gcc aac Phe Gly Ala Gly Gly Tyr Tyr Cys Gln Pro Leu Arg His Gly Ala Asn 325 330 335	1008
atc gtg ctg cac tcg gcg agc aag tgg atc ggc ggg cac ggc aac ggc Ile Val Leu His Ser Ala Ser Lys Trp Ile Gly Gly His Gly Asn Gly 340 345 350	1056
atc ggc ggg gtc atc gtg gac ggc ggg aac ttc gac tgg ggc agc ggg Ile Gly Gly Val Ile Val Asp Gly Gly Asn Phe Asp Trp Gly Ser Gly 355 360 365	1104
cgg tat ccg ctg atg acc gag ccc tcg ccg agt tat cac ggg ctg aag Arg Tyr Pro Leu Met Thr Glu Pro Ser Pro Ser Tyr His Gly Leu Lys 370 375 380	1152
ttc tgg gag acg ttc ggg gaa ggc aac ggg ctg ggg ctg ccg aac atc Phe Trp Glu Thr Phe Gly Glu Gly Asn Gly Leu Gly Leu Pro Asn Ile 385 390 395 400	1200
gcc ttc atc acc cgc gcc cgc acc gag ggg ctg cgc gac ctg gga acg Ala Phe Ile Thr Arg Ala Arg Thr Glu Gly Leu Arg Asp Leu Gly Thr 405 410 415	1248
acc ctg gcg ccg cag cag gcg tgg cag ttt ctg caa ggc ctt gaa acc Thr Leu Ala Pro Gln Gln Ala Trp Gln Phe Leu Gln Gly Leu Glu Thr 420 425 430	1296
ctg agc ctg cgc gcc gag cgc cac gcc gag aac acc ctg gcg ctg gcg Leu Ser Leu Arg Ala Glu Arg His Ala Glu Asn Thr Leu Ala Leu Ala 435 440 445	1344
cac tgg ctc atc agc cac ccg gac gtg aag cag gtc act tac ccc ggc His Trp Leu Ile Ser His Pro Asp Val Lys Gln Val Thr Tyr Pro Gly 450 455 460	1392
ctg agc aac cac ccc cac tac gac cgg gcg cag acc tac ttg ccg cgc Leu Ser Asn His Pro His Tyr Asp Arg Ala Gln Thr Tyr Leu Pro Arg 465 470 475 480	1440
ggg gcg ggc gcg gtg ctc acc ttc gag ctg cgc ggg ggc cgg gcg gcg Gly Ala Gly Ala Val Leu Thr Phe Glu Leu Arg Gly Gly Arg Ala Ala 485 490 495	1488

ggc gaa gcg ttt att cgc tcg gtc aag ctc gcg cag cac gtc gcc aac 1536
 Gly Glu Ala Phe Ile Arg Ser Val Lys Leu Ala Gln His Val Ala Asn
 500 505 510

gtg ggc gac acc cgc acg ctg gtc att cat ccg gcg agc acc acc cac 1584
 Val Gly Asp Thr Arg Thr Leu Val Ile His Pro Ala Ser Thr Thr His
 515 520 525

agc cag ctc gac gag gtg acg cag acg aac gcc ggg gtc acg ccg ggc 1632
 Ser Gln Leu Asp Glu Val Thr Gln Thr Asn Ala Gly Val Thr Pro Gly
 530 535 540

ctc atc cgg gtg tcg gtg ggc atc gag cac gta gac gac atc cgc gag 1680
 Leu Ile Arg Val Ser Val Gly Ile Glu His Val Asp Asp Ile Arg Glu
 545 550 555 560

gac ttc gcg cag gcc ctg gcg agc gct ggg gag cgg gcg tga 1722
 Asp Phe Ala Gln Ala Leu Ala Ser Ala Gly Glu Arg Ala
 565 570

<210> 36

<211> 573

<212> PRT

<213> Deinococcus radiodurans

<400> 36

Val Ala Phe Pro Cys Gly Gln Ala Gly Asn Lys Ile Thr Arg Pro Gly
 1 5 10 15

Gln Cys Val Asn Gly Gly Arg Ala Arg Ser Ala Pro Ser Lys Phe Arg
 20 25 30

Leu Asp Pro Leu Pro Ala Ser Ala Leu Leu Phe Glu Glu Leu Pro Gln
 35 40 45

Gln Glu Pro Pro Thr Ser Glu Arg Pro Arg Asp Leu Ala Arg Arg Arg
 50 55 60

Arg Gly Asn Arg Thr Pro Ser Arg His Gly Ala Lys Ala Ser Pro Leu
 65 70 75 80

Gly Val Ser Thr Met Ser Arg Arg Ala Gly Pro Ser Gly Lys Ala Thr
 85 90 95

Arg Met Thr Ile Phe Lys Cys Pro Phe Ser Ile His Ser Arg Gln Gly
 100 105 110

Glu Cys Arg Asp Trp Arg Pro Arg Thr Cys Phe Pro Arg Gly Ala Ala
 115 120 125

Thr Met Thr Asp Thr Lys Gln Pro Gln Pro Leu His Phe Glu Thr Leu
 130 135 140

Gln Val His Ala Gly Gln Arg Pro Asp Pro Val Thr Gly Ala Gln Gln
 145 150 155 160

Thr Pro Ile Tyr Ala Thr Asn Ser Tyr Val Phe Glu Ser Pro Glu His
 165 170 175

Ala Ala Asp Leu Phe Gly Leu Arg Gln Phe Gly Asn Ile Tyr Ser Arg
 180 185 190

Ile Met Asn Pro Thr Asn Asp Val Phe Glu Gln Arg Val Ala Ala Leu
 195 200 205

Glu Gly Gly Val Gly Ala Leu Ser Val Ser Ser Gly His Ala Gly Gln
 210 215 220

Leu Val Thr Leu Leu Thr Leu Ala Gln Ala Gly Asp Asn Ile Val Ser
 225 230 235 240

Ser Pro Asn Leu Tyr Gly Gly Thr Val Asn Gln Phe Arg Val Thr Leu
 245 250 255

Lys Arg Leu Gly Ile Glu Val Arg Phe Thr Ser Lys Asp Glu Arg Pro
 260 265 270

Glu Glu Phe Ala Ala Leu Ile Asp Glu Arg Thr Arg Ala Val Tyr Leu
 275 280 285

Glu Thr Ile Gly Asn Pro Ala Leu Asn Ile Pro Asp Phe Glu Gly Val
 290 295 300

Ala Lys Val Ala His Glu His Gly Val Ala Val Val Val Asp Asn Thr
 305 310 315 320

Phe Gly Ala Gly Gly Tyr Tyr Cys Gln Pro Leu Arg His Gly Ala Asn
 325 330 335

Ile Val Leu His Ser Ala Ser Lys Trp Ile Gly Gly His Gly Asn Gly
 340 345 350

Ile Gly Gly Val Ile Val Asp Gly Gly Asn Phe Asp Trp Gly Ser Gly
 355 360 365

Arg Tyr Pro Leu Met Thr Glu Pro Ser Pro Ser Tyr His Gly Leu Lys
 370 375 380

Phe Trp Glu Thr Phe Gly Glu Gly Asn Gly Leu Gly Leu Pro Asn Ile
 385 390 395 400

Ala Phe Ile Thr Arg Ala Arg Thr Glu Gly Leu Arg Asp Leu Gly Thr
 405 410 415

Thr Leu Ala Pro Gln Gln Ala Trp Gln Phe Leu Gln Gly Leu Glu Thr
 420 425 430

Leu Ser Leu Arg Ala Glu Arg His Ala Glu Asn Thr Leu Ala Leu Ala
 435 440 445

His Trp Leu Ile Ser His Pro Asp Val Lys Gln Val Thr Tyr Pro Gly
 450 455 460

Leu Ser Asn His Pro His Tyr Asp Arg Ala Gln Thr Tyr Leu Pro Arg
 465 470 475 480

Gly Ala Gly Ala Val Leu Thr Phe Glu Leu Arg Gly Gly Arg Ala Ala
 485 490 495

Gly Glu Ala Phe Ile Arg Ser Val Lys Leu Ala Gln His Val Ala Asn
 500 505 510

Val Gly Asp Thr Arg Thr Leu Val Ile His Pro Ala Ser Thr Thr His
 515 520 525

Ser Gln Leu Asp Glu Val Thr Gln Thr Asn Ala Gly Val Thr Pro Gly
 530 535 540

Leu Ile Arg Val Ser Val Gly Ile Glu His Val Asp Asp Ile Arg Glu
 545 550 555 560

Asp Phe Ala Gln Ala Leu Ala Ser Ala Gly Glu Arg Ala
 565 570

<210> 37

<211> 1284

<212> DNA

<213> Rhodobacter capsulatus

<220>

<221> CDS

<222> (1) .. (1284)

<400> 37

atg acc gac cag gcc ttt gac acg ctg caa att cac gcg ggc gcc gaa	48
Met Thr Asp Gln Ala Phe Asp Thr Leu Gln Ile His Ala Gly Ala Glu	
1 5 10 15	
ccc gat ccc gcg acg ggc gcg cgg cag gtg ccg att tac cag acc acc	96
Pro Asp Pro Ala Thr Gly Ala Arg Gln Val Pro Ile Tyr Gln Thr Thr	
20 25 30	
tcc tat gtc ttc aag gac gcc gac cat gcc gcg cgc ctg ttc ggg ctg	144
Ser Tyr Val Phe Lys Asp Ala Asp His Ala Ala Arg Leu Phe Gly Leu	
35 40 45	
cag gag gtg ggc tat atc tat tcc cgc ctg acc aac ccg acc gtt tcg	192
Gln Glu Val Gly Tyr Ile Tyr Ser Arg Leu Thr Asn Pro Thr Val Ser	
50 55 60	
gca ctg gcc gcc cgc gtt gcg gcg ctt gaa ggc ggc gtg ggc gcg gtc	240
Ala Leu Ala Ala Arg Val Ala Ala Leu Glu Gly Gly Val Gly Ala Val	
65 70 75 80	
tgc tgc tcg tcc ggc cat gcg gcg cag atc atg gcg ctg ttt ccg ctg	288
Cys Cys Ser Ser Gly His Ala Ala Gln Ile Met Ala Leu Phe Pro Leu	
85 90 95	
atg ggg ccg ggg ctg aac atc gtc gcc tcg acc ccg ctt tac ggc ggc	336
Met Gly Pro Gly Leu Asn Ile Val Ala Ser Thr Arg Leu Tyr Gly Gly	
100 105 110	
acg atc acc cag ttc agc cag acc atc aaa cgc ttc ggc tgg tcc tgc	384
Thr Ile Thr Gln Phe Ser Gln Thr Ile Lys Arg Phe Gly Trp Ser Cys	
115 120 125	
acc ttt gtc gat ttc gac gat ctg gcg gcg ctc gag gcc gcg gtg gat	432
Thr Phe Val Asp Phe Asp Leu Ala Ala Leu Glu Ala Ala Val Asp	
130 135 140	
gac aac acc cgg gcg atc ttt tgc gaa tcg atc tcg aac ccg ggc ggc	480
Asp Asn Thr Arg Ala Ile Phe Cys Glu Ser Ile Ser Asn Pro Gly Gly	
145 150 155 160	
tac atc acc gac ctg ccc gcc gtc gcg gcg gtg gcg aac aag gtc ggc	528
Tyr Ile Thr Asp Leu Pro Ala Val Ala Ala Val Ala Asn Lys Val Gly	
165 170 175	

ctg ccg ctc att gtc gac aac acg ctg gcc tcg cct tat ctc tgc cgc	576
Leu Pro Leu Ile Val Asp Asn Thr Leu Ala Ser Pro Tyr Leu Cys Arg	
180 185 190	
ccg atc gag cat ggc gcg acg ctg gtt gtc cat tcc gcc acg aaa tac	624
Pro Ile Glu His Gly Ala Thr Leu Val Val His Ser Ala Thr Lys Tyr	
195 200 205	
ctg acc ggc aac ggc acg gtg acg ggc ggg gtg atc gtc gat tcg ggc	672
Leu Thr Gly Asn Gly Thr Val Thr Gly Gly Val Ile Val Asp Ser Gly	
210 215 220	
aag ttc gac tgg tcg gcc tcg ggc aag ttc ccc agc ctt tcg gcg ccc	720
Lys Phe Asp Trp Ser Ala Ser Gly Lys Phe Pro Ser Leu Ser Ala Pro	
225 230 235 240	
gaa ccc gcc tat cac ggg ctg aag ttc cac gag gca ctc ggc ccg atg	768
Glu Pro Ala Tyr His Gly Leu Lys Phe His Glu Ala Leu Gly Pro Met	
245 250 255	
gcc ttc acc ttc cat tcg atc gcc gtc ggg ctg cgc gat ctg ggc atg	816
Ala Phe Thr Phe His Ser Ile Ala Val Gly Leu Arg Asp Leu Gly Met	
260 265 270	
acg atg aac ccg cag ggc gcg cat tac acg ctg atg ggg atc gag acg	864
Thr Met Asn Pro Gln Gly Ala His Tyr Thr Leu Met Gly Ile Glu Thr	
275 280 285	
ctc agc ctg cgc atg gac aag cac gtc gcc aat gcg aag gcg gtg gcg	912
Leu Ser Leu Arg Met Asp Lys His Val Ala Asn Ala Lys Ala Val Ala	
290 295 300	
gaa tgg ctg gcc aaa gac ccg cgc atc gac ttc gtc acc tgg gcc ggg	960
Glu Trp Leu Ala Lys Asp Pro Arg Ile Asp Phe Val Thr Trp Ala Gly	
305 310 315 320	
ctg ccc tcc tcg ccc tgg cac gaa cgc gcc gag cgg ctt tgc ccg aag	1008
Leu Pro Ser Ser Pro Trp His Glu Arg Ala Glu Arg Leu Cys Pro Lys	
325 330 335	
ggg gcg ggg gcg ctt ttc acc gtc gcg gtc aag ggc ggc tat gag gcc	1056
Gly Ala Gly Ala Leu Phe Thr Val Ala Val Lys Gly Gly Tyr Glu Ala	
340 345 350	
tgc gtg aaa ttg gtc aac aat ctc aag ctg ttc agc cat gtg gca aac	1104
Cys Val Lys Leu Val Asn Asn Leu Lys Leu Phe Ser His Val Ala Asn	
355 360 365	
ctg ggc gac gcg cgc tcg ctg atc atc cat tcg gcc tcg acc acg cac	1152
Leu Gly Asp Ala Arg Ser Leu Ile Ile His Ser Ala Ser Thr Thr His	
370 375 380	
cgt cag ctg acc gag gaa cag cag atc aag gcg ggg gcg gcg ccg aat	1200
Arg Gln Leu Thr Glu Glu Gln Gln Ile Lys Ala Gly Ala Ala Pro Asn	
385 390 395 400	
gtg gtg cgg ctc tcg atc ggg atc gag aat gcc gcc gat ctg atc gcc	1248
Val Val Arg Leu Ser Ile Gly Ile Glu Asn Ala Ala Asp Leu Ile Ala	
405 410 415	

gat ctg gat cag gct ctg gcc gcc gcc acc gcc tga
 Asp Leu Asp Gln Ala Leu Ala Ala Ala Thr Ala
 420 425

1284

<210> 38

<211> 427

<212> PRT

<213> Rhodobacter capsulatus

<400> 38

Met Thr Asp Gln Ala Phe Asp Thr Leu Gln Ile His Ala Gly Ala Glu
 1 5 10 15

Pro Asp Pro Ala Thr Gly Ala Arg Gln Val Pro Ile Tyr Gln Thr Thr
 20 25 30

Ser Tyr Val Phe Lys Asp Ala Asp His Ala Ala Arg Leu Phe Gly Leu
 35 40 45

Gln Glu Val Gly Tyr Ile Tyr Ser Arg Leu Thr Asn Pro Thr Val Ser
 50 55 60

Ala Leu Ala Ala Arg Val Ala Ala Leu Glu Gly Gly Val Gly Ala Val
 65 70 75 80

Cys Cys Ser Ser Gly His Ala Ala Gln Ile Met Ala Leu Phe Pro Leu
 85 90 95

Met Gly Pro Gly Leu Asn Ile Val Ala Ser Thr Arg Leu Tyr Gly Gly
 100 105 110

Thr Ile Thr Gln Phe Ser Gln Thr Ile Lys Arg Phe Gly Trp Ser Cys
 115 120 125

Thr Phe Val Asp Phe Asp Asp Leu Ala Ala Leu Glu Ala Ala Val Asp
 130 135 140

Asp Asn Thr Arg Ala Ile Phe Cys Glu Ser Ile Ser Asn Pro Gly Gly
 145 150 155 160

Tyr Ile Thr Asp Leu Pro Ala Val Ala Ala Val Ala Asn Lys Val Gly
 165 170 175

Leu Pro Leu Ile Val Asp Asn Thr Leu Ala Ser Pro Tyr Leu Cys Arg
 180 185 190

Pro Ile Glu His Gly Ala Thr Leu Val Val His Ser Ala Thr Lys Tyr
 195 200 205

Leu Thr Gly Asn Gly Thr Val Thr Gly Gly Val Ile Val Asp Ser Gly
 210 215 220

Lys Phe Asp Trp Ser Ala Ser Gly Lys Phe Pro Ser Leu Ser Ala Pro
 225 230 235 240

Glu Pro Ala Tyr His Gly Leu Lys Phe His Glu Ala Leu Gly Pro Met
 245 250 255

Ala Phe Thr Phe His Ser Ile Ala Val Gly Leu Arg Asp Leu Gly Met
 260 265 270

Thr Met Asn Pro Gln Gly Ala His Tyr Thr Leu Met Gly Ile Glu Thr
 275 280 285

Leu Ser Leu Arg Met Asp Lys His Val Ala Asn Ala Lys Ala Val Ala
 290 295 300

Glu Trp Leu Ala Lys Asp Pro Arg Ile Asp Phe Val Thr Trp Ala Gly
 305 310 315 320

Leu Pro Ser Ser Pro Trp His Glu Arg Ala Glu Arg Leu Cys Pro Lys
 325 330 335

Gly Ala Gly Ala Leu Phe Thr Val Ala Val Lys Gly Gly Tyr Glu Ala
 340 345 350

Cys Val Lys Leu Val Asn Asn Leu Lys Leu Phe Ser His Val Ala Asn
 355 360 365

Leu Gly Asp Ala Arg Ser Leu Ile Ile His Ser Ala Ser Thr Thr His
 370 375 380

Arg Gln Leu Thr Glu Glu Gln Gln Ile Lys Ala Gly Ala Ala Pro Asn
 385 390 395 400

Val Val Arg Leu Ser Ile Gly Ile Glu Asn Ala Ala Asp Leu Ile Ala
 405 410 415

Asp Leu Asp Gln Ala Leu Ala Ala Ala Thr Ala
 420 425

<210> 39

<211> 1269

<212> DNA

<213> Pasteurella multocida

<220>

<221> CDS

<222> (1) .. (1269)

<400> 39

atg gaa ttt gca aca aaa tgt cta cat gcc ggt tat aca ccg aaa aat	48
Met Glu Phe Ala Thr Lys Cys Leu His Ala Gly Tyr Thr Pro Lys Asn	
1 5 10 15	
ggg gag cct cgt gtt caa ccg atc gta caa agt acc act ttt acc tac	96
Gly Glu Pro Arg Val Gln Pro Ile Val Gln Ser Thr Thr Phe Thr Tyr	
20 25 30	
gat tcc gcc gaa gaa att ggt aag tta ttt gat tta caa gcg gct ggc	144
Asp Ser Ala Glu Glu Ile Gly Lys Leu Phe Asp Leu Gln Ala Ala Gly	
35 40 45	
tat ttt tac acc cgc ctt tca aat cct act acc aat gcg gca gaa gaa	192
Tyr Phe Tyr Thr Arg Leu Ser Asn Pro Thr Thr Asn Ala Ala Glu Glu	
50 55 60	
aaa att acc gca ctt gaa ggc ggt gta gca acc atg tgt acc gca tca	240
Lys Ile Thr Ala Leu Glu Gly Gly Val Ala Thr Met Cys Thr Ala Ser	
65 70 75 80	
ggg caa gcc gcc gtg ttt tac gcg atg ctc aat att tta caa gcc ggt	288
Gly Gln Ala Ala Val Phe Tyr Ala Met Leu Asn Ile Leu Gln Ala Gly	
85 90 95	
gat cac ttt att tct tca tcg tat gtt tac ggt ggt agc tac aac tta	336
Asp His Phe Ile Ser Ser Ser Tyr Val Tyr Gly Gly Ser Tyr Asn Leu	
100 105 110	
ttt gca cat acc ttc aaa aaa atg gga att gag gtc act ttt gtg gat	384
Phe Ala His Thr Phe Lys Lys Met Gly Ile Glu Val Thr Phe Val Asp	
115 120 125	
caa gat tta cct ctt gag gaa tta aaa aaa gct att cgc cca aat acg	432
Gln Asp Leu Pro Leu Glu Glu Leu Lys Lys Ala Ile Arg Pro Asn Thr	

130	135	140	
aaa gcc att ttt gcc gaa act att gcc aat ccc gca tta cgc gtg ttg			480
Lys Ala Ile Phe Ala Glu Thr Ile Ala Asn Pro Ala Leu Arg Val Leu			
145	150	155	160
gat att gaa aag ttt gtt gca ctt gcg aag gca gca caa gcc cct tta			528
Asp Ile Glu Lys Phe Val Ala Leu Ala Lys Ala Ala Gln Ala Pro Leu			
	165	170	175
tta gtt gac aat act ttt gca acc ccg tat ttt tgt cgc cct atc gaa			576
Leu Val Asp Asn Thr Phe Ala Thr Pro Tyr Phe Cys Arg Pro Ile Glu			
	180	185	190
ttt ggt gct aac gtg gta att cat agt acg tca aaa tat tta gat ggg			624
Phe Gly Ala Asn Val Val Ile His Ser Thr Ser Lys Tyr Leu Asp Gly			
	195	200	205
cat gcg att gcg ttg gga ggt tgc atc aca gat ggc ggg aat ttt gat			672
His Ala Ile Ala Leu Gly Gly Ser Ile Thr Asp Gly Gly Asn Phe Asp			
	210	215	220
tgg aat aat ggt aaa ttc cca caa tta agc aca cct gat caa act tat			720
Trp Asn Asn Gly Lys Phe Pro Gln Leu Ser Thr Pro Asp Gln Thr Tyr			
	225	230	235
cac ggt tta gtt tat acc gaa acc ttt gtt cca gcc gct tat att gtc			768
His Gly Leu Val Tyr Thr Glu Thr Phe Val Pro Ala Ala Tyr Ile Val			
	245	250	255
aaa gcc cgt gtg caa tta atg cgt gat tta ggt gcc aca cca gca cca			816
Lys Ala Arg Val Gln Leu Met Arg Asp Leu Gly Ala Thr Pro Ala Pro			
	260	265	270
caa aat agt ttc ttg ctc aat gtg ggc atg gaa act ctt gca ctg cgt			864
Gln Asn Ser Phe Leu Leu Asn Val Gly Met Glu Thr Leu Ala Leu Arg			
	275	280	285
atg caa cgt cat tat gaa aat gca caa gcg gtc gcc gaa ttt tta gaa			912
Met Gln Arg His Tyr Glu Asn Ala Gln Ala Val Ala Glu Phe Leu Glu			
	290	295	300
aat cat cca caa gtg gca aaa gtg agt tat ccg ggc ttg gca agt tca			960
Asn His Pro Gln Val Ala Lys Val Ser Tyr Pro Gly Leu Ala Ser Ser			
	305	310	315
cct gat cat gca cta aaa caa aaa tat tta cca aac ggt tta tgt ggt			1008
Pro Asp His Ala Leu Lys Gln Lys Tyr Leu Pro Asn Gly Leu Cys Gly			
	325	330	335
gtg att tcc ttt gaa att aga ggg gga aga gaa act gca gca aaa tgg			1056
Val Ile Ser Phe Glu Ile Arg Gly Gly Arg Glu Thr Ala Ala Lys Trp			
	340	345	350
ctg aat gcg cta caa ctg gct tct cgt gaa gtc cat gta gcg gat att			1104
Leu Asn Ala Leu Gln Leu Ala Ser Arg Glu Val His Val Ala Asp Ile			
	355	360	365
cgc act tgt gct tta cat ccg gcg acg tca aca cac cgt caa tta agt			1152
Arg Thr Cys Ala Leu His Pro Ala Thr Ser Thr His Arg Gln Leu Ser			

370

375

380

gag gct gaa tta gaa aaa gtg ggg att tct gcg ggt tta att cgt ctt 1200
 Glu Ala Glu Leu Glu Lys Val Gly Ile Ser Ala Gly Leu Ile Arg Leu
 385 390 395 400

tct tgc ggt att gaa agt atc caa gat att ttg gct gac tta gaa caa 1248
 Ser Cys Gly Ile Glu Ser Ile Gln Asp Ile Leu Ala Asp Leu Glu Gln
 405 410 415

gca ttc cac gcg gca aaa taa 1269
 Ala Phe His Ala Ala Lys
 420

<210> 40

<211> 422

<212> PRT

<213> Pasteurella multocida

<400> 40

Met Glu Phe Ala Thr Lys Cys Leu His Ala Gly Tyr Thr Pro Lys Asn
 1 5 10 15

Gly Glu Pro Arg Val Gln Pro Ile Val Gln Ser Thr Thr Phe Thr Tyr
 20 25 30

Asp Ser Ala Glu Glu Ile Gly Lys Leu Phe Asp Leu Gln Ala Ala Gly
 35 40 45

Tyr Phe Tyr Thr Arg Leu Ser Asn Pro Thr Thr Asn Ala Ala Glu Glu
 50 55 60

Lys Ile Thr Ala Leu Glu Gly Gly Val Ala Thr Met Cys Thr Ala Ser
 65 70 75 80

Gly Gln Ala Ala Val Phe Tyr Ala Met Leu Asn Ile Leu Gln Ala Gly
 85 90 95

Asp His Phe Ile Ser Ser Ser Tyr Val Tyr Gly Gly Ser Tyr Asn Leu
 100 105 110

Phe Ala His Thr Phe Lys Lys Met Gly Ile Glu Val Thr Phe Val Asp
 115 120 125

Gln Asp Leu Pro Leu Glu Glu Leu Lys Lys Ala Ile Arg Pro Asn Thr

130

135

140

Lys Ala Ile Phe Ala Glu Thr Ile Ala Asn Pro Ala Leu Arg Val Leu
 145 150 155 160

Asp Ile Glu Lys Phe Val Ala Leu Ala Lys Ala Ala Gln Ala Pro Leu
 165 170 175

Leu Val Asp Asn Thr Phe Ala Thr Pro Tyr Phe Cys Arg Pro Ile Glu
 180 185 190

Phe Gly Ala Asn Val Val Ile His Ser Thr Ser Lys Tyr Leu Asp Gly
 195 200 205

His Ala Ile Ala Leu Gly Gly Ser Ile Thr Asp Gly Gly Asn Phe Asp
 210 215 220

Trp Asn Asn Gly Lys Phe Pro Gln Leu Ser Thr Pro Asp Gln Thr Tyr
 225 230 235 240

His Gly Leu Val Tyr Thr Glu Thr Phe Val Pro Ala Ala Tyr Ile Val
 245 250 255

Lys Ala Arg Val Gln Leu Met Arg Asp Leu Gly Ala Thr Pro Ala Pro
 260 265 270

Gln Asn Ser Phe Leu Leu Asn Val Gly Met Glu Thr Leu Ala Leu Arg
 275 280 285

Met Gln Arg His Tyr Glu Asn Ala Gln Ala Val Ala Glu Phe Leu Glu
 290 295 300

Asn His Pro Gln Val Ala Lys Val Ser Tyr Pro Gly Leu Ala Ser Ser
 305 310 315 320

Pro Asp His Ala Leu Lys Gln Lys Tyr Leu Pro Asn Gly Leu Cys Gly
 325 330 335

Val Ile Ser Phe Glu Ile Arg Gly Gly Arg Glu Thr Ala Ala Lys Trp
 340 345 350

Leu Asn Ala Leu Gln Leu Ala Ser Arg Glu Val His Val Ala Asp Ile
 355 360 365

Arg Thr Cys Ala Leu His Pro Ala Thr Ser Thr His Arg Gln Leu Ser

370

375

380

Glu Ala Glu Leu Glu Lys Val Gly Ile Ser Ala Gly Leu Ile Arg Leu
 385 390 395 400

Ser Cys Gly Ile Glu Ser Ile Gln Asp Ile Leu Ala Asp Leu Glu Gln
 405 410 415

Ala Phe His Ala Ala Lys
 420

<210> 41

<211> 1266

<212> DNA

<213> Clostridium difficile

<220>

<221> CDS

<222> (1) .. (1266)

<400> 41
 atg tat aat aaa gaa aca ata tgt gtg caa gga aat tat aaa cca ggt 48
 Met Tyr Asn Lys Glu Thr Ile Cys Val Gln Gly Asn Tyr Lys Pro Gly
 1 5 10 15
 aat gga gaa cca aga gta cta cct tta tat caa agt aca act ttt aaa 96
 Asn Gly Glu Pro Arg Val Leu Pro Leu Tyr Gln Ser Thr Thr Phe Lys
 20 25 30
 tat agc agt ata gac caa ctt gct gaa tta ttt gat tta aaa gtt gat 144
 Tyr Ser Ser Ile Asp Gln Leu Ala Glu Leu Phe Asp Leu Lys Val Asp
 35 40 45
 gga cat ata tat tca aga ata agc aat cct act att caa gct ttt gaa 192
 Gly His Ile Tyr Ser Arg Ile Ser Asn Pro Thr Ile Gln Ala Phe Glu
 50 55 60
 gaa aaa ata agt tta cta gag ggt gga gta tct tct gta gct gta tca 240
 Glu Lys Ile Ser Leu Leu Glu Gly Gly Val Ser Ser Val Ala Val Ser
 65 70 75 80
 tca ggg caa tct gca aat atg ttg gca gtt tta aat ata tgt aaa tca 288
 Ser Gly Gln Ser Ala Asn Met Leu Ala Val Leu Asn Ile Cys Lys Ser
 85 90 95
 gga gat agt ata ctt tgt tct tca aaa gta tat gga gga aca ttc aat 336

Gly	Asp	Ser	Ile	Leu	Cys	Ser	Ser	Lys	Val	Tyr	Gly	Gly	Thr	Phe	Asn	
			100					105					110			
tta	cta	gga	cct	agt	ctt	aaa	aaa	ttt	ggt	ata	gat	tta	ata	tcg	ttt	384
Leu	Leu	Gly	Pro	Ser	Leu	Lys	Lys	Phe	Gly	Ile	Asp	Leu	Ile	Ser	Phe	
		115					120					125				
gac	tta	gat	tca	agt	gaa	gat	gag	ata	gta	gaa	ctt	gca	aag	gaa	aat	432
Asp	Leu	Asp	Ser	Ser	Glu	Asp	Glu	Ile	Val	Glu	Leu	Ala	Lys	Glu	Asn	
	130					135					140					
act	aag	gtt	gtg	ttt	gca	gaa	aca	ctt	gca	aat	cca	act	ctt	gaa	gtc	480
Thr	Lys	Val	Val	Phe	Ala	Glu	Thr	Leu	Ala	Asn	Pro	Thr	Leu	Glu	Val	
145					150					155					160	
ata	gat	ttt	gaa	aaa	ata	gca	aat	gta	gct	aag	aga	att	aat	gtt	cca	528
Ile	Asp	Phe	Glu	Lys	Ile	Ala	Asn	Val	Ala	Lys	Arg	Ile	Asn	Val	Pro	
			165					170					175			
ttt	att	gtt	gat	aat	tca	tta	gca	tct	cca	gtg	ctt	tgt	aac	cct	tta	576
Phe	Ile	Val	Asp	Asn	Ser	Leu	Ala	Ser	Pro	Val	Leu	Cys	Asn	Pro	Leu	
		180						185					190			
aag	tat	gga	gca	aat	ata	gtt	act	cat	tct	acc	aca	aaa	tat	tta	gat	624
Lys	Tyr	Gly	Ala	Asn	Ile	Val	Thr	His	Ser	Thr	Thr	Lys	Tyr	Leu	Asp	
	195						200					205				
ggg	cat	gct	tca	agt	gtt	gga	gga	att	ata	gtg	gat	ggg	gga	aac	ttt	672
Gly	His	Ala	Ser	Ser	Val	Gly	Gly	Ile	Ile	Val	Asp	Gly	Gly	Asn	Phe	
	210					215					220					
aac	tgg	gat	aat	gga	aaa	ttt	cca	gaa	tta	gtt	gag	cca	gac	cca	aca	720
Asn	Trp	Asp	Asn	Gly	Lys	Phe	Pro	Glu	Leu	Val	Glu	Pro	Asp	Pro	Thr	
225				230						235					240	
tat	cat	ggg	ata	agc	tat	act	caa	aaa	ttt	gga	aat	gcc	gca	tat	gca	768
Tyr	His	Gly	Ile	Ser	Tyr	Thr	Gln	Lys	Phe	Gly	Asn	Ala	Ala	Tyr	Ala	
			245					250					255			
act	aaa	gca	aga	gtt	cag	ttg	ctt	aga	gac	tat	gga	aat	tgt	tta	agc	816
Thr	Lys	Ala	Arg	Val	Gln	Leu	Leu	Arg	Asp	Tyr	Gly	Asn	Cys	Leu	Ser	
		260						265					270			
cca	ttc	aat	gcg	tat	ctt	act	aat	tta	aat	gtt	gaa	aca	cta	cat	ctt	864
Pro	Phe	Asn	Ala	Tyr	Leu	Thr	Asn	Leu	Asn	Val	Glu	Thr	Leu	His	Leu	
		275					280					285				
aga	atg	gag	aga	cat	agt	gaa	aat	gca	ctt	aaa	ata	gct	aga	ttt	tta	912
Arg	Met	Glu	Arg	His	Ser	Glu	Asn	Ala	Leu	Lys	Ile	Ala	Arg	Phe	Leu	
	290					295					300					
gaa	aaa	cat	gaa	aat	gta	gat	tgg	att	aat	tac	cca	gga	ctt	gaa	gat	960
Glu	Lys	His	Glu	Asn	Val	Asp	Trp	Ile	Asn	Tyr	Pro	Gly	Leu	Glu	Asp	
305				310					315					320		
aac	aag	tat	tat	gag	aat	gcc	aaa	aag	tat	tta	tca	aga	gga	tgt	agt	1008
Asn	Lys	Tyr	Tyr	Glu	Asn	Ala	Lys	Lys	Tyr	Leu	Ser	Arg	Gly	Cys	Ser	
			325						330					335		
ggg	gtt	tta	tca	ttt	gga	gta	aga	ggg	ggg	tta	gaa	aat	gcc	aaa	aaa	1056

Gly Val Leu Ser Phe Gly Val Arg Gly Gly Leu Glu Asn Ala Lys Lys
 340 345 350

ttt gtg gaa aaa tta cag ata gca tct ttg gtt aca cat gtt tca gat 1104
 Phe Val Glu Lys Leu Gln Ile Ala Ser Leu Val Thr His Val Ser Asp
 355 360 365

gta aga act tgt gtt ata cat cca gct tca act act cat aga caa tta 1152
 Val Arg Thr Cys Val Ile His Pro Ala Ser Thr Thr His Arg Gln Leu
 370 375 380

aca gaa gaa caa tta att gca tct gga gta ttg cct tca cta ata aga 1200
 Thr Glu Glu Gln Leu Ile Ala Ser Gly Val Leu Pro Ser Leu Ile Arg
 385 390 395 400

tta tct gtt gga ata gaa aat gta gag gat tta ata gct gat tta aat 1248
 Leu Ser Val Gly Ile Glu Asn Val Glu Asp Leu Ile Ala Asp Leu Asn
 405 410 415

caa gct tta aat ttc taa 1266
 Gln Ala Leu Asn Phe
 420

<210> 42
 <211> 421
 <212> PRT
 <213> Clostridium difficile

<400> 42

Met Tyr Asn Lys Glu Thr Ile Cys Val Gln Gly Asn Tyr Lys Pro Gly
 1 5 10 15

Asn Gly Glu Pro Arg Val Leu Pro Leu Tyr Gln Ser Thr Thr Phe Lys
 20 25 30

Tyr Ser Ser Ile Asp Gln Leu Ala Glu Leu Phe Asp Leu Lys Val Asp
 35 40 45

Gly His Ile Tyr Ser Arg Ile Ser Asn Pro Thr Ile Gln Ala Phe Glu
 50 55 60

Glu Lys Ile Ser Leu Leu Glu Gly Gly Val Ser Ser Val Ala Val Ser
 65 70 75 80

Ser Gly Gln Ser Ala Asn Met Leu Ala Val Leu Asn Ile Cys Lys Ser
 85 90 95

Gly Asp Ser Ile Leu Cys Ser Ser Lys Val Tyr Gly Gly Thr Phe Asn
 100 105 110

Leu Leu Gly Pro Ser Leu Lys Lys Phe Gly Ile Asp Leu Ile Ser Phe
 115 120 125

Asp Leu Asp Ser Ser Glu Asp Glu Ile Val Glu Leu Ala Lys Glu Asn
 130 135 140

Thr Lys Val Val Phe Ala Glu Thr Leu Ala Asn Pro Thr Leu Glu Val
 145 150 155 160

Ile Asp Phe Glu Lys Ile Ala Asn Val Ala Lys Arg Ile Asn Val Pro
 165 170 175

Phe Ile Val Asp Asn Ser Leu Ala Ser Pro Val Leu Cys Asn Pro Leu
 180 185 190

Lys Tyr Gly Ala Asn Ile Val Thr His Ser Thr Thr Lys Tyr Leu Asp
 195 200 205

Gly His Ala Ser Ser Val Gly Gly Ile Ile Val Asp Gly Gly Asn Phe
 210 215 220

Asn Trp Asp Asn Gly Lys Phe Pro Glu Leu Val Glu Pro Asp Pro Thr
 225 230 235 240

Tyr His Gly Ile Ser Tyr Thr Gln Lys Phe Gly Asn Ala Ala Tyr Ala
 245 250 255

Thr Lys Ala Arg Val Gln Leu Leu Arg Asp Tyr Gly Asn Cys Leu Ser
 260 265 270

Pro Phe Asn Ala Tyr Leu Thr Asn Leu Asn Val Glu Thr Leu His Leu
 275 280 285

Arg Met Glu Arg His Ser Glu Asn Ala Leu Lys Ile Ala Arg Phe Leu
 290 295 300

Glu Lys His Glu Asn Val Asp Trp Ile Asn Tyr Pro Gly Leu Glu Asp
 305 310 315 320

Asn Lys Tyr Tyr Glu Asn Ala Lys Lys Tyr Leu Ser Arg Gly Cys Ser
 325 330 335

Gly Val Leu Ser Phe Gly Val Arg Gly Gly Leu Glu Asn Ala Lys Lys
 340 345 350

Phe Val Glu Lys Leu Gln Ile Ala Ser Leu Val Thr His Val Ser Asp
 355 360 365

Val Arg Thr Cys Val Ile His Pro Ala Ser Thr Thr His Arg Gln Leu
 370 375 380

Thr Glu Glu Gln Leu Ile Ala Ser Gly Val Leu Pro Ser Leu Ile Arg
 385 390 395 400

Leu Ser Val Gly Ile Glu Asn Val Glu Asp Leu Ile Ala Asp Leu Asn
 405 410 415

Gln Ala Leu Asn Phe
 420

<210> 43

<211> 1272

<212> DNA

<213> Campylobacter jejuni

<220>

<221> CDS

<222> (1) .. (1272)

<400> 43

atg aat ttc aat aaa gaa act tta gca tta cac gga gct tat aat ttt	48
Met Asn Phe Asn Lys Glu Thr Leu Ala Leu His Gly Ala Tyr Asn Phe	
1 5 10 15	
gat act caa aga agt att agt gtg cct ata tat caa aac act gcg tat	96
Asp Thr Gln Arg Ser Ile Ser Val Pro Ile Tyr Gln Asn Thr Ala Tyr	
20 25 30	
aat ttt gaa aat ttg gat caa gct gca gca agg ttt aat ctt caa gaa	144
Asn Phe Glu Asn Leu Asp Gln Ala Ala Ala Arg Phe Asn Leu Gln Glu	
35 40 45	
ctt ggc aat att tac tca aga ctt agc aat cct aca agc gat gtt tta	192
Leu Gly Asn Ile Tyr Ser Arg Leu Ser Asn Pro Thr Ser Asp Val Leu	
50 55 60	

gga caa aga ctt gct aat gtc gaa gga ggg gct ttt gga att cct gtt	240
Gly Gln Arg Leu Ala Asn Val Glu Gly Gly Ala Phe Gly Ile Pro Val	
65 70 75 80	
gct agc ggt atg gca gct tgt ttt tat gct ctt atc aat tta gca agt	288
Ala Ser Gly Met Ala Ala Cys Phe Tyr Ala Leu Ile Asn Leu Ala Ser	
85 90 95	
tcg gga gat aat gtc gcg tat tcg aac aaa att tat ggt ggg act caa	336
Ser Gly Asp Asn Val Ala Tyr Ser Asn Lys Ile Tyr Gly Gly Thr Gln	
100 105 110	
act tta att tct cac aca ctt aaa aat ttt ggc ata gaa gct agg gaa	384
Thr Leu Ile Ser His Thr Leu Lys Asn Phe Gly Ile Glu Ala Arg Glu	
115 120 125	
ttt gat atc gat gat tta gat agc ttg gaa aaa gtt ata gat caa aac	432
Phe Asp Ile Asp Asp Leu Asp Ser Leu Glu Lys Val Ile Asp Gln Asn	
130 135 140	
aca aaa gcg att ttt ttc gaa agt ctt tca aat cct caa att gcc ata	480
Thr Lys Ala Ile Phe Phe Glu Ser Leu Ser Asn Pro Gln Ile Ala Ile	
145 150 155 160	
gct gat ata gaa aaa ata aac caa ata gca aaa aaa cat aaa atc gtt	528
Ala Asp Ile Glu Lys Ile Asn Gln Ile Ala Lys Lys His Lys Ile Val	
165 170 175	
agc att tgt gat aat acc gtt gct act cct ttc tta ctc caa cct ttt	576
Ser Ile Cys Asp Asn Thr Val Ala Thr Pro Phe Leu Leu Gln Pro Phe	
180 185 190	
aaa cat ggc gtg gat gta atc gtg cat agt tta agt aaa tat gta agc	624
Lys His Gly Val Asp Val Ile Val His Ser Leu Ser Lys Tyr Val Ser	
195 200 205	
ggg caa ggc act gct ttg ggt gga gca ctt ata gaa aga aaa gat tta	672
Gly Gln Gly Thr Ala Leu Gly Gly Ala Leu Ile Glu Arg Lys Asp Leu	
210 215 220	
aac gac ttg ctt aaa aat aac gat aga tat aaa gct ttt aac act cct	720
Asn Asp Leu Leu Lys Asn Asn Asp Arg Tyr Lys Ala Phe Asn Thr Pro	
225 230 235 240	
gat cca agt tat cat gga ctg aat tta aat aca ctt gat ttg ccg att	768
Asp Pro Ser Tyr His Gly Leu Asn Leu Asn Thr Leu Asp Leu Pro Ile	
245 250 255	
ttt agt att aga gtc atc atc act tgg ctt aga gat cta gga gct agc	816
Phe Ser Ile Arg Val Ile Ile Thr Trp Leu Arg Asp Leu Gly Ala Ser	
260 265 270	
tta gca cct caa aat gct tgg tta ctt tta caa gga ctt gaa acc ttg	864
Leu Ala Pro Gln Asn Ala Trp Leu Leu Leu Gln Gly Leu Glu Thr Leu	
275 280 285	
gca gtg cgt ata gaa aaa cac agt caa aat gct gaa aaa gtt gcg aat	912
Ala Val Arg Ile Glu Lys His Ser Gln Asn Ala Glu Lys Val Ala Asn	
290 295 300	

ttt tta aat tct cat cct gat atc aag ggc gta aat tat cct act tta 960
 Phe Leu Asn Ser His Pro Asp Ile Lys Gly Val Asn Tyr Pro Thr Leu
 305 310 315 320

gca agt aat gct tat cat aat tta ttt aaa aaa tat ttt gat aaa aat 1008
 Ala Ser Asn Ala Tyr His Asn Leu Phe Lys Lys Tyr Phe Asp Lys Asn
 325 330 335

ttt gct agc ggg ctt tta agc ttt gaa gct aaa gat tat gag cat gct 1056
 Phe Ala Ser Gly Leu Leu Ser Phe Glu Ala Lys Asp Tyr Glu His Ala
 340 345 350

aga aga att tgt gat aaa act caa ctt ttc tta ctt gct gca aat ttg 1104
 Arg Arg Ile Cys Asp Lys Thr Gln Leu Phe Leu Leu Ala Ala Asn Leu
 355 360 365

ggg gat agc aag tct ttg atc atc cat cct gct tct act act cat tcg 1152
 Gly Asp Ser Lys Ser Leu Ile Ile His Pro Ala Ser Thr Thr His Ser
 370 375 380

caa cta agc gaa gaa gaa ctc caa aaa gca ggc att acg aaa gct act 1200
 Gln Leu Ser Glu Glu Glu Leu Gln Lys Ala Gly Ile Thr Lys Ala Thr
 385 390 395 400

ata cgc tta agc ata gga ctt gaa aat agc gat gat ttg ata gcg gat 1248
 Ile Arg Leu Ser Ile Gly Leu Glu Asn Ser Asp Asp Leu Ile Ala Asp
 405 410 415

tta aaa caa gct ata gaa agt taa 1272
 Leu Lys Gln Ala Ile Glu Ser
 420

<210> 44

<211> 423

<212> PRT

<213> Campylobacter jejuni

<400> 44

Met Asn Phe Asn Lys Glu Thr Leu Ala Leu His Gly Ala Tyr Asn Phe
 1 5 10 15

Asp Thr Gln Arg Ser Ile Ser Val Pro Ile Tyr Gln Asn Thr Ala Tyr
 20 25 30

Asn Phe Glu Asn Leu Asp Gln Ala Ala Ala Arg Phe Asn Leu Gln Glu
 35 40 45

Leu Gly Asn Ile Tyr Ser Arg Leu Ser Asn Pro Thr Ser Asp Val Leu
 50 55 60

Gly Gln Arg Leu Ala Asn Val Glu Gly Gly Ala Phe Gly Ile Pro Val
65 70 75 80

Ala Ser Gly Met Ala Ala Cys Phe Tyr Ala Leu Ile Asn Leu Ala Ser
85 90 95

Ser Gly Asp Asn Val Ala Tyr Ser Asn Lys Ile Tyr Gly Gly Thr Gln
100 105 110

Thr Leu Ile Ser His Thr Leu Lys Asn Phe Gly Ile Glu Ala Arg Glu
115 120 125

Phe Asp Ile Asp Asp Leu Asp Ser Leu Glu Lys Val Ile Asp Gln Asn
130 135 140

Thr Lys Ala Ile Phe Phe Glu Ser Leu Ser Asn Pro Gln Ile Ala Ile
145 150 155 160

Ala Asp Ile Glu Lys Ile Asn Gln Ile Ala Lys Lys His Lys Ile Val
165 170 175

Ser Ile Cys Asp Asn Thr Val Ala Thr Pro Phe Leu Leu Gln Pro Phe
180 185 190

Lys His Gly Val Asp Val Ile Val His Ser Leu Ser Lys Tyr Val Ser
195 200 205

Gly Gln Gly Thr Ala Leu Gly Gly Ala Leu Ile Glu Arg Lys Asp Leu
210 215 220

Asn Asp Leu Leu Lys Asn Asn Asp Arg Tyr Lys Ala Phe Asn Thr Pro
225 230 235 240

Asp Pro Ser Tyr His Gly Leu Asn Leu Asn Thr Leu Asp Leu Pro Ile
245 250 255

Phe Ser Ile Arg Val Ile Ile Thr Trp Leu Arg Asp Leu Gly Ala Ser
260 265 270

Leu Ala Pro Gln Asn Ala Trp Leu Leu Leu Gln Gly Leu Glu Thr Leu
275 280 285

Ala Val Arg Ile Glu Lys His Ser Gln Asn Ala Glu Lys Val Ala Asn
290 295 300

Phe Leu Asn Ser His Pro Asp Ile Lys Gly Val Asn Tyr Pro Thr Leu
305 310 315 320

Ala Ser Asn Ala Tyr His Asn Leu Phe Lys Lys Tyr Phe Asp Lys Asn
325 330 335

Phe Ala Ser Gly Leu Leu Ser Phe Glu Ala Lys Asp Tyr Glu His Ala
340 345 350

Arg Arg Ile Cys Asp Lys Thr Gln Leu Phe Leu Leu Ala Ala Asn Leu
355 360 365

Gly Asp Ser Lys Ser Leu Ile Ile His Pro Ala Ser Thr Thr His Ser
370 375 380

Gln Leu Ser Glu Glu Glu Leu Gln Lys Ala Gly Ile Thr Lys Ala Thr
385 390 395 400

Ile Arg Leu Ser Ile Gly Leu Glu Asn Ser Asp Asp Leu Ile Ala Asp
405 410 415

Leu Lys Gln Ala Ile Glu Ser
420

<210> 45

<211> 1041

<212> DNA

<213> Streptococcus pneumoniae

<220>

<221> CDS

<222> (1)..(1041)

<400> 45

ttg agg aaa cca ggg aac att tat act cgt atc acc aat cct aca aca
Leu Arg Lys Pro Gly Asn Ile Tyr Thr Arg Ile Thr Asn Pro Thr Thr
1 5 10 15

48

gct gcc ctt gaa ggt ggt gtt gaa gcg cta gca aca gca tca ggt atg
Ala Ala Leu Glu Gly Gly Val Glu Ala Leu Ala Thr Ala Ser Gly Met
20 25 30

96

act gca gtg act tat acg att ttg gcg att gcc cat gct ggt gac cat	144
Thr Ala Val Thr Tyr Thr Ile Leu Ala Ile Ala His Ala Gly Asp His	
35 40 45	
gta gtg gct gct tcg act att tac ggt gga acc ttc aat ctt ttg aaa	192
Val Val Ala Ala Ser Thr Ile Tyr Gly Gly Thr Phe Asn Leu Leu Lys	
50 55 60	
gaa ccc ctt cct cgt tat ggt atc aca aca acc ttt ttc gat att gat	240
Glu Pro Leu Pro Arg Tyr Gly Ile Thr Thr Thr Phe Phe Asp Ile Asp	
65 70 75 80	
aat ttg gag gaa gta gaa gca gct atc aaa gac aat acc aag ctt gtc	288
Asn Leu Glu Glu Val Glu Ala Ala Ile Lys Asp Asn Thr Lys Leu Val	
85 90 95	
ttg att gaa acc ttg ggt aac ccc ttg att aat att cca gac ctg gaa	336
Leu Ile Glu Thr Leu Gly Asn Pro Leu Ile Asn Ile Pro Asp Leu Glu	
100 105 110	
aaa ctg gca gag att gct cat aaa cat caa atc cca ctt gtg tca gac	384
Lys Leu Ala Glu Ile Ala His Lys His Gln Ile Pro Leu Val Ser Asp	
115 120 125	
aat act ttt gca aca cct tat ttg att aac gtc ttc tct cat ggc gtt	432
Asn Thr Phe Ala Thr Pro Tyr Leu Ile Asn Val Phe Ser His Gly Val	
130 135 140	
gac att gcc att cac tct gtg act aag ttt atc ggt ggg cat ggt aca	480
Asp Ile Ala Ile His Ser Val Thr Lys Phe Ile Gly Gly His Gly Thr	
145 150 155 160	
act att gga gga ata att gtc gat agt ggt cgt ttt gac tgg acg gct	528
Thr Ile Gly Gly Ile Ile Val Asp Ser Gly Arg Phe Asp Trp Thr Ala	
165 170 175	
tca ggg aaa ttc cct caa ttt gtt gac gag ggt cca agc tgc cac aat	576
Ser Gly Lys Phe Pro Gln Phe Val Asp Glu Gly Pro Ser Cys His Asn	
180 185 190	
ttg agc tat act cgt gat gtg ggt gca gca gcc ttt att ata gct gtt	624
Leu Ser Tyr Thr Arg Asp Val Gly Ala Ala Ala Phe Ile Ile Ala Val	
195 200 205	
cga gtt caa ttg ctt cgt gat aca ggt gca gcc ttg tca cca ttc aat	672
Arg Val Gln Leu Leu Arg Asp Thr Gly Ala Ala Leu Ser Pro Phe Asn	
210 215 220	
gct ttc ctc ttg cta caa aga ctt gaa acc tct tca ctt cgt gtg gaa	720
Ala Phe Leu Leu Leu Gln Arg Leu Glu Thr Ser Ser Leu Arg Val Glu	
225 230 235 240	
cgc cat gta caa aat gct gag aca att gtt gat ttt ctt gtc aac cat	768
Arg His Val Gln Asn Ala Glu Thr Ile Val Asp Phe Leu Val Asn His	
245 250 255	
cct aag gta gaa aag gta aat tat cca aaa ctt gca gat agt cct tat	816
Pro Lys Val Glu Lys Val Asn Tyr Pro Lys Leu Ala Asp Ser Pro Tyr	
260 265 270	

cat gcc ttg gct gag aaa tac ttg cca aaa ggt gtc ggt tca atc ttt 864
 His Ala Leu Ala Glu Lys Tyr Leu Pro Lys Gly Val Gly Ser Ile Phe
 275 280 285

acc ttc cac gtc aaa ggt ggc gag gaa gaa gca cgc aag gtc att gat 912
 Thr Phe His Val Lys Gly Gly Glu Glu Glu Ala Arg Lys Val Ile Asp
 290 295 300

aat tta gaa atc ttt tct gac ctt gca aac gcg gca gat gct aaa tcg 960
 Asn Leu Glu Ile Phe Ser Asp Leu Ala Asn Ala Ala Asp Ala Lys Ser
 305 310 315 320

ctt gtt gtc cat cca gca aca acc act cac ggt caa ttg tca gaa aaa 1008
 Leu Val Val His Pro Ala Thr Thr Thr His Gly Gln Leu Ser Glu Lys
 325 330 335

gac cta gaa gca gca ggt gtc aca cca aac taa 1041
 Asp Leu Glu Ala Ala Gly Val Thr Pro Asn
 340 345

<210> 46

<211> 346

<212> PRT

<213> Streptococcus pneumoniae

<400> 46

Leu Arg Lys Pro Gly Asn Ile Tyr Thr Arg Ile Thr Asn Pro Thr Thr
 1 5 10 15

Ala Ala Leu Glu Gly Gly Val Glu Ala Leu Ala Thr Ala Ser Gly Met
 20 25 30

Thr Ala Val Thr Tyr Thr Ile Leu Ala Ile Ala His Ala Gly Asp His
 35 40 45

Val Val Ala Ala Ser Thr Ile Tyr Gly Gly Thr Phe Asn Leu Leu Lys
 50 55 60

Glu Pro Leu Pro Arg Tyr Gly Ile Thr Thr Thr Phe Phe Asp Ile Asp
 65 70 75 80

Asn Leu Glu Glu Val Glu Ala Ala Ile Lys Asp Asn Thr Lys Leu Val
 85 90 95

Leu Ile Glu Thr Leu Gly Asn Pro Leu Ile Asn Ile Pro Asp Leu Glu
 100 105 110

Lys Leu Ala Glu Ile Ala His Lys His Gln Ile Pro Leu Val Ser Asp
 115 120 125

Asn Thr Phe Ala Thr Pro Tyr Leu Ile Asn Val Phe Ser His Gly Val
 130 135 140

Asp Ile Ala Ile His Ser Val Thr Lys Phe Ile Gly Gly His Gly Thr
 145 150 155 160

Thr Ile Gly Gly Ile Ile Val Asp Ser Gly Arg Phe Asp Trp Thr Ala
 165 170 175

Ser Gly Lys Phe Pro Gln Phe Val Asp Glu Gly Pro Ser Cys His Asn
 180 185 190

Leu Ser Tyr Thr Arg Asp Val Gly Ala Ala Ala Phe Ile Ile Ala Val
 195 200 205

Arg Val Gln Leu Leu Arg Asp Thr Gly Ala Ala Leu Ser Pro Phe Asn
 210 215 220

Ala Phe Leu Leu Leu Gln Arg Leu Glu Thr Ser Ser Leu Arg Val Glu
 225 230 235 240

Arg His Val Gln Asn Ala Glu Thr Ile Val Asp Phe Leu Val Asn His
 245 250 255

Pro Lys Val Glu Lys Val Asn Tyr Pro Lys Leu Ala Asp Ser Pro Tyr
 260 265 270

His Ala Leu Ala Glu Lys Tyr Leu Pro Lys Gly Val Gly Ser Ile Phe
 275 280 285

Thr Phe His Val Lys Gly Gly Glu Glu Glu Ala Arg Lys Val Ile Asp
 290 295 300

Asn Leu Glu Ile Phe Ser Asp Leu Ala Asn Ala Ala Asp Ala Lys Ser
 305 310 315 320

Leu Val Val His Pro Ala Thr Thr Thr His Gly Gln Leu Ser Glu Lys
 325 330 335

Asp Leu Glu Ala Ala Gly Val Thr Pro Asn
 340 345

<210> 47

<211> 1335

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1) .. (1335)

<400> 47

atg cca tct cat ttc gat act gtt caa cta cac gcc ggc caa gag aac	48
Met Pro Ser His Phe Asp Thr Val Gln Leu His Ala Gly Gln Glu Asn	
1 5 10 15	
cct ggt gac aat gct cac aga tcc aga gct gta cca att tac gcc acc	96
Pro Gly Asp Asn Ala His Arg Ser Arg Ala Val Pro Ile Tyr Ala Thr	
20 25 30	
act tct tat gtt ttc gaa aac tct aag cat ggt tcg caa ttg ttt ggt	144
Thr Ser Tyr Val Phe Glu Asn Ser Lys His Gly Ser Gln Leu Phe Gly	
35 40 45	
cta gaa gtt cca ggt tac gtc tat tcc cgt ttc caa aac cca acc agt	192
Leu Glu Val Pro Gly Tyr Val Tyr Ser Arg Phe Gln Asn Pro Thr Ser	
50 55 60	
aat gtt ttg gaa gaa aga att gct gct tta gaa ggt ggt gct gct gct	240
Asn Val Leu Glu Glu Arg Ile Ala Ala Leu Glu Gly Gly Ala Ala Ala	
65 70 75 80	
ttg gct gtt tcc tcc ggt caa gcc gct caa acc ctt gcc atc caa ggt	288
Leu Ala Val Ser Ser Gly Gln Ala Ala Gln Thr Leu Ala Ile Gln Gly	
85 90 95	
ttg gca cac act ggt gac aac atc gtt tcc act tct tac tta tac ggt	336
Leu Ala His Thr Gly Asp Asn Ile Val Ser Thr Ser Tyr Leu Tyr Gly	
100 105 110	
ggt act tat aac cag ttc aaa atc tcg ttc aaa aga ttt ggt atc gag	384
Gly Thr Tyr Asn Gln Phe Lys Ile Ser Phe Lys Arg Phe Gly Ile Glu	
115 120 125	
gct aga ttt gtt gaa ggt gac aat cca gaa gaa ttc gaa aag gtc ttt	432
Ala Arg Phe Val Glu Gly Asp Asn Pro Glu Glu Phe Glu Lys Val Phe	
130 135 140	
gat gaa aga acc aag gct gtt tat ttg gaa acc att ggt aat cca aag	480
Asp Glu Arg Thr Lys Ala Val Tyr Leu Glu Thr Ile Gly Asn Pro Lys	

145	150	155	160	
tac aat gtt ccg gat ttt gaa aaa att gtt gca att gct cac aaa cac				528
Tyr Asn Val Pro Asp Phe Glu Lys Ile Val Ala Ile Ala His Lys His				
	165	170	175	
ggt att cca gtt gtc gtt gac aac aca ttt ggt gcc ggt ggt tac ttc				576
Gly Ile Pro Val Val Val Asp Asn Thr Phe Gly Ala Gly Gly Tyr Phe				
	180	185	190	
tgt cag cca att aaa tac ggt gct gat att gta aca cat tct gct acc				624
Cys Gln Pro Ile Lys Tyr Gly Ala Asp Ile Val Thr His Ser Ala Thr				
	195	200	205	
aaa tgg att ggt ggt cat ggt act act atc ggt ggt att att gtt gac				672
Lys Trp Ile Gly Gly His Gly Thr Thr Ile Gly Gly Ile Ile Val Asp				
	210	215	220	
tct ggt aag ttc cca tgg aag gac tac cca gaa aag ttc cct caa ttc				720
Ser Gly Lys Phe Pro Trp Lys Asp Tyr Pro Glu Lys Phe Pro Gln Phe				
	225	230	235	240
tct caa cct gcc gaa gga tat cac ggt act atc tac aat gaa gcc tac				768
Ser Gln Pro Ala Glu Gly Tyr His Gly Thr Ile Tyr Asn Glu Ala Tyr				
	245	250	255	
ggt aac ttg gca tac atc gtt cat gtt aga act gaa cta tta aga gat				816
Gly Asn Leu Ala Tyr Ile Val His Val Arg Thr Glu Leu Leu Arg Asp				
	260	265	270	
ttg ggt cca ttg atg aac cca ttt gcc tct ttc ttg cta cta caa ggt				864
Leu Gly Pro Leu Met Asn Pro Phe Ala Ser Phe Leu Leu Leu Gln Gly				
	275	280	285	
gtt gaa aca tta tct ttg aga gct gaa aga cac ggt gaa aat gaa ttg				912
Val Glu Thr Leu Ser Leu Arg Ala Glu Arg His Gly Glu Asn Ala Leu				
	290	295	300	
aag tta gcc aaa tgg tta gaa caa tcc cca tac gta tct tgg gtt tca				960
Lys Leu Ala Lys Trp Leu Glu Gln Ser Pro Tyr Val Ser Trp Val Ser				
	305	310	315	320
tac cct ggt tta gca tct cat tct cat cat gaa aat gct aag aag tat				1008
Tyr Pro Gly Leu Ala Ser His Ser His His Glu Asn Ala Lys Lys Tyr				
	325	330	335	
cta tct aac ggt ttc ggt ggt gtc tta tct ttc ggt gta aaa gac tta				1056
Leu Ser Asn Gly Phe Gly Gly Val Leu Ser Phe Gly Val Lys Asp Leu				
	340	345	350	
cca aat gcc gac aag gaa act gac cca ttc aaa ctt tct ggt gct caa				1104
Pro Asn Ala Asp Lys Glu Thr Asp Pro Phe Lys Leu Ser Gly Ala Gln				
	355	360	365	
gtt gtt gac aat tta aag ctt gcc tct aac ttg gcc aat gtt ggt gat				1152
Val Val Asp Asn Leu Lys Leu Ala Ser Asn Leu Ala Asn Val Gly Asp				
	370	375	380	
gcc aag acc tta gtc att gct cca tac ttc act acc cac aaa caa tta				1200
Ala Lys Thr Leu Val Ile Ala Pro Tyr Phe Thr Thr His Lys Gln Leu				

385 390 395 400
 aat gac aaa gaa aag ttg gca tct ggt gtt acc aag gac tta att cgt 1248
 Asn Asp Lys Glu Lys Leu Ala Ser Gly Val Thr Lys Asp Leu Ile Arg
 405 410 415
 gtc tct gtt ggt atc gaa ttt att gat gac att att gca gac ttc cag 1296
 Val Ser Val Gly Ile Glu Phe Ile Asp Asp Ile Ile Ala Asp Phe Gln
 420 425 430
 caa tct ttt gaa act gtt ttc gct ggc caa aaa cca tga 1335
 Gln Ser Phe Glu Thr Val Phe Ala Gly Gln Lys Pro
 435 440

<210> 48

<211> 444

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 48

Met Pro Ser His Phe Asp Thr Val Gln Leu His Ala Gly Gln Glu Asn
 1 5 10 15
 Pro Gly Asp Asn Ala His Arg Ser Arg Ala Val Pro Ile Tyr Ala Thr
 20 25 30
 Thr Ser Tyr Val Phe Glu Asn Ser Lys His Gly Ser Gln Leu Phe Gly
 35 40 45
 Leu Glu Val Pro Gly Tyr Val Tyr Ser Arg Phe Gln Asn Pro Thr Ser
 50 55 60
 Asn Val Leu Glu Glu Arg Ile Ala Ala Leu Glu Gly Gly Ala Ala Ala
 65 70 75 80
 Leu Ala Val Ser Ser Gly Gln Ala Ala Gln Thr Leu Ala Ile Gln Gly
 85 90 95
 Leu Ala His Thr Gly Asp Asn Ile Val Ser Thr Ser Tyr Leu Tyr Gly
 100 105 110
 Gly Thr Tyr Asn Gln Phe Lys Ile Ser Phe Lys Arg Phe Gly Ile Glu
 115 120 125
 Ala Arg Phe Val Glu Gly Asp Asn Pro Glu Glu Phe Glu Lys Val Phe

130

135

140

Asp Glu Arg Thr Lys Ala Val Tyr Leu Glu Thr Ile Gly Asn Pro Lys
 145 150 155 160

Tyr Asn Val Pro Asp Phe Glu Lys Ile Val Ala Ile Ala His Lys His
 165 170 175

Gly Ile Pro Val Val Val Asp Asn Thr Phe Gly Ala Gly Gly Tyr Phe
 180 185 190

Cys Gln Pro Ile Lys Tyr Gly Ala Asp Ile Val Thr His Ser Ala Thr
 195 200 205

Lys Trp Ile Gly Gly His Gly Thr Thr Ile Gly Gly Ile Ile Val Asp
 210 215 220

Ser Gly Lys Phe Pro Trp Lys Asp Tyr Pro Glu Lys Phe Pro Gln Phe
 225 230 235 240

Ser Gln Pro Ala Glu Gly Tyr His Gly Thr Ile Tyr Asn Glu Ala Tyr
 245 250 255

Gly Asn Leu Ala Tyr Ile Val His Val Arg Thr Glu Leu Leu Arg Asp
 260 265 270

Leu Gly Pro Leu Met Asn Pro Phe Ala Ser Phe Leu Leu Leu Gln Gly
 275 280 285

Val Glu Thr Leu Ser Leu Arg Ala Glu Arg His Gly Glu Asn Ala Leu
 290 295 300

Lys Leu Ala Lys Trp Leu Glu Gln Ser Pro Tyr Val Ser Trp Val Ser
 305 310 315 320

Tyr Pro Gly Leu Ala Ser His Ser His His Glu Asn Ala Lys Lys Tyr
 325 330 335

Leu Ser Asn Gly Phe Gly Gly Val Leu Ser Phe Gly Val Lys Asp Leu
 340 345 350

Pro Asn Ala Asp Lys Glu Thr Asp Pro Phe Lys Leu Ser Gly Ala Gln
 355 360 365

Val Val Asp Asn Leu Lys Leu Ala Ser Asn Leu Ala Asn Val Gly Asp

370

375

380

Ala Lys Thr Leu Val Ile Ala Pro Tyr Phe Thr Thr His Lys Gln Leu
 385 390 395 400

Asn Asp Lys Glu Lys Leu Ala Ser Gly Val Thr Lys Asp Leu Ile Arg
 405 410 415

Val Ser Val Gly Ile Glu Phe Ile Asp Asp Ile Ile Ala Asp Phe Gln
 420 425 430

Gln Ser Phe Glu Thr Val Phe Ala Gly Gln Lys Pro
 435 440

<210> 49

<211> 1335

<212> DNA

<213> Kluyveromyces lactis

<220>

<221> CDS

<222> (1)..(1335)

<400> 49

atg cca tct cac ttc gat act ttg caa ttg cac gct ggt caa gaa aag 48
 Met Pro Ser His Phe Asp Thr Leu Gln Leu His Ala Gly Gln Glu Lys
 1 5 10 15

act gct gat gct cat aac cca aga gcc gtc cca att tac gct acc act 96
 Thr Ala Asp Ala His Asn Pro Arg Ala Val Pro Ile Tyr Ala Thr Thr
 20 25 30

tct tac gtc ttc aac gac tct aag cat ggt gct caa ttg ttc ggt tta 144
 Ser Tyr Val Phe Asn Asp Ser Lys His Gly Ala Gln Leu Phe Gly Leu
 35 40 45

gaa act cca ggt tac att tac tct cgt att atg aac cct act cta gac 192
 Glu Thr Pro Gly Tyr Ile Tyr Ser Arg Ile Met Asn Pro Thr Leu Asp
 50 55 60

gtc ttg gaa aag aga ttg gca gcc tta gaa ggt ggt att gct gct ttg 240
 Val Leu Glu Lys Arg Leu Ala Ala Leu Glu Gly Gly Ile Ala Ala Leu
 65 70 75 80

gct act tct tct ggc caa gct gct caa acc ttg gct gtc act ggt ttg 288

Ala Thr Ser Ser Gly Gln Ala Ala Gln Thr Leu Ala Val Thr Gly Leu	
85 90 95	
gcc cac act ggt gac aat att gtc tct acc tct ttc tta tac ggt ggt	336
Ala His Thr Gly Asp Asn Ile Val Ser Thr Ser Phe Leu Tyr Gly Gly	
100 105 110	
act tat aac caa ttc aag gtt gcc ttc aag aga tta gga att gaa gct	384
Thr Tyr Asn Gln Phe Lys Val Ala Phe Lys Arg Leu Gly Ile Glu Ala	
115 120 125	
aga ttt gtc gat ggt gac aag cca gaa gac ttc gaa aag ttg ttc gat	432
Arg Phe Val Asp Gly Asp Lys Pro Glu Asp Phe Glu Lys Leu Phe Asp	
130 135 140	
gaa aag act aag gct ctc tat ctg gaa tct atc ggt aat cct aag tac	480
Glu Lys Thr Lys Ala Leu Tyr Leu Glu Ser Ile Gly Asn Pro Lys Tyr	
145 150 155 160	
aat gtc cca gac ttc gaa aag att gtt gct gtt gct cat aag cat ggt	528
Asn Val Pro Asp Phe Glu Lys Ile Val Ala Val Ala His Lys His Gly	
165 170 175	
atc cca gtt gtt gtt gac aac act ttc ggt gcc ggt ggt ttc ttc tgc	576
Ile Pro Val Val Val Asp Asn Thr Phe Gly Ala Gly Gly Phe Phe Cys	
180 185 190	
caa cct atc aaa tac ggt gct gat atc gtt act cac tct gct acc aag	624
Gln Pro Ile Lys Tyr Gly Ala Asp Ile Val Thr His Ser Ala Thr Lys	
195 200 205	
tgg atc ggt ggt cat ggt gtc acc gtt ggt ggt gtc atc att gac tct	672
Trp Ile Gly Gly His Gly Val Thr Val Gly Gly Val Ile Ile Asp Ser	
210 215 220	
ggt aag ttc cca tgg aag gat tac ccg gaa aag ttc cct caa ttc tct	720
Gly Lys Phe Pro Trp Lys Asp Tyr Pro Glu Lys Phe Pro Gln Phe Ser	
225 230 235 240	
cag cca tct gaa ggt tat cat ggt ttg atc ttc aat gat gcc ttt ggt	768
Gln Pro Ser Glu Gly Tyr His Gly Leu Ile Phe Asn Asp Ala Phe Gly	
245 250 255	
cca gct gct ttc att ggt cat gta aga acc gaa ttg cta aga gat tta	816
Pro Ala Ala Phe Ile Gly His Val Arg Thr Glu Leu Leu Arg Asp Leu	
260 265 270	
ggt cca gtg ttg agt cca ttc gct ggt ttc ttg ttg tta cag ggt ctt	864
Gly Pro Val Leu Ser Pro Phe Ala Gly Phe Leu Leu Leu Gln Gly Leu	
275 280 285	
gaa act ttg tct cta aga ggt gaa aga cac ggt tcc aac gct ttg aag	912
Glu Thr Leu Ser Leu Arg Gly Glu Arg His Gly Ser Asn Ala Leu Lys	
290 295 300	
ttg gct caa tac ttg gaa agt tct cca tac gtt tca tgg gtc tct tac	960
Leu Ala Gln Tyr Leu Glu Ser Ser Pro Tyr Val Ser Trp Val Ser Tyr	
305 310 315 320	
cca ggt ttg cca tct cac tct cac cac gaa aac gct aag aaa tac ttg	1008

Pro Gly Leu Pro Ser His Ser His His Glu Asn Ala Lys Lys Tyr Leu
 325 330 335

gaa aat ggt ttc ggt ggt gtt tta tcc ttc ggt gtc aaa gat ttg cct 1056
 Glu Asn Gly Phe Gly Gly Val Leu Ser Phe Gly Val Lys Asp Leu Pro
 340 345 350

aac gct tcc gag gaa tct gat cca ttc aag gct tct ggt gcc caa gtt 1104
 Asn Ala Ser Glu Glu Ser Asp Pro Phe Lys Ala Ser Gly Ala Gln Val
 355 360 365

gtt gac aac ttg aag ctg gct tct aac ttg gca aac gtt ggt gac tcc 1152
 Val Asp Asn Leu Lys Leu Ala Ser Asn Leu Ala Asn Val Gly Asp Ser
 370 375 380

aag acc ttg gtc att gct cca tac ttc act aca cat caa caa ttg acc 1200
 Lys Thr Leu Val Ile Ala Pro Tyr Phe Thr Thr His Gln Gln Leu Thr
 385 390 395 400

gac gaa gaa aag tta gct tct ggt gtt acc aag gac ttg atc cgt gtt 1248
 Asp Glu Glu Lys Leu Ala Ser Gly Val Thr Lys Asp Leu Ile Arg Val
 405 410 415

tct gtt ggt act gaa ttc att gac gac att att gct gac ttt gaa gca 1296
 Ser Val Gly Thr Glu Phe Ile Asp Asp Ile Ile Ala Asp Phe Glu Ala
 420 425 430

tct ttc gct act gtc ttc aat ggc caa aaa cct gaa taa 1335
 Ser Phe Ala Thr Val Phe Asn Gly Gln Lys Pro Glu
 435 440

<210> 50

<211> 444

<212> PRT

<213> Kluyveromyces lactis

<400> 50

Met Pro Ser His Phe Asp Thr Leu Gln Leu His Ala Gly Gln Glu Lys
 1 5 10 15

Thr Ala Asp Ala His Asn Pro Arg Ala Val Pro Ile Tyr Ala Thr Thr
 20 25 30

Ser Tyr Val Phe Asn Asp Ser Lys His Gly Ala Gln Leu Phe Gly Leu
 35 40 45

Glu Thr Pro Gly Tyr Ile Tyr Ser Arg Ile Met Asn Pro Thr Leu Asp
 50 55 60

Val Leu Glu Lys Arg Leu Ala Ala Leu Glu Gly Gly Ile Ala Ala Leu
65 70 75 80

Ala Thr Ser Ser Gly Gln Ala Ala Gln Thr Leu Ala Val Thr Gly Leu
85 90 95

Ala His Thr Gly Asp Asn Ile Val Ser Thr Ser Phe Leu Tyr Gly Gly
100 105 110

Thr Tyr Asn Gln Phe Lys Val Ala Phe Lys Arg Leu Gly Ile Glu Ala
115 120 125

Arg Phe Val Asp Gly Asp Lys Pro Glu Asp Phe Glu Lys Leu Phe Asp
130 135 140

Glu Lys Thr Lys Ala Leu Tyr Leu Glu Ser Ile Gly Asn Pro Lys Tyr
145 150 155 160

Asn Val Pro Asp Phe Glu Lys Ile Val Ala Val Ala His Lys His Gly
165 170 175

Ile Pro Val Val Val Asp Asn Thr Phe Gly Ala Gly Gly Phe Phe Cys
180 185 190

Gln Pro Ile Lys Tyr Gly Ala Asp Ile Val Thr His Ser Ala Thr Lys
195 200 205

Trp Ile Gly Gly His Gly Val Thr Val Gly Gly Val Ile Ile Asp Ser
210 215 220

Gly Lys Phe Pro Trp Lys Asp Tyr Pro Glu Lys Phe Pro Gln Phe Ser
225 230 235 240

Gln Pro Ser Glu Gly Tyr His Gly Leu Ile Phe Asn Asp Ala Phe Gly
245 250 255

Pro Ala Ala Phe Ile Gly His Val Arg Thr Glu Leu Leu Arg Asp Leu
260 265 270

Gly Pro Val Leu Ser Pro Phe Ala Gly Phe Leu Leu Leu Gln Gly Leu
275 280 285

Glu Thr Leu Ser Leu Arg Gly Glu Arg His Gly Ser Asn Ala Leu Lys
290 295 300

Leu Ala Gln Tyr Leu Glu Ser Ser Pro Tyr Val Ser Trp Val Ser Tyr
 305 310 315 320

Pro Gly Leu Pro Ser His Ser His His Glu Asn Ala Lys Lys Tyr Leu
 325 330 335

Glu Asn Gly Phe Gly Gly Val Leu Ser Phe Gly Val Lys Asp Leu Pro
 340 345 350

Asn Ala Ser Glu Glu Ser Asp Pro Phe Lys Ala Ser Gly Ala Gln Val
 355 360 365

Val Asp Asn Leu Lys Leu Ala Ser Asn Leu Ala Asn Val Gly Asp Ser
 370 375 380

Lys Thr Leu Val Ile Ala Pro Tyr Phe Thr Thr His Gln Gln Leu Thr
 385 390 395 400

Asp Glu Glu Lys Leu Ala Ser Gly Val Thr Lys Asp Leu Ile Arg Val
 405 410 415

Ser Val Gly Thr Glu Phe Ile Asp Asp Ile Ile Ala Asp Phe Glu Ala
 420 425 430

Ser Phe Ala Thr Val Phe Asn Gly Gln Lys Pro Glu
 435 440

<210> 51

<211> 1323

<212> DNA

<213> Candida albicans

<220>

<221> CDS

<222> (1)..(1323)

<400> 51

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 Met Pro Ser His Phe Asp Thr Leu Gln Leu His Ala Gly Gln Pro Val
 1 5 10 15

gaa	aaa	cca	cac	caa	cca	aga	gcc	cca	cca	att	tat	gca	acc	acc	tcc	96
Glu	Lys	Pro	His	Gln	Pro	Arg	Ala	Pro	Pro	Ile	Tyr	Ala	Thr	Thr	Ser	
			20				25						30			
tat	gtt	ttc	aat	gac	tct	aaa	cac	ggg	gct	caa	tta	ttt	ggg	tta	gaa	144
Tyr	Val	Phe	Asn	Asp	Ser	Lys	His	Gly	Ala	Gln	Leu	Phe	Gly	Leu	Glu	
		35					40					45				
acc	cca	gga	tac	att	tac	tcc	aga	att	atg	aat	cca	aca	aac	gat	gtg	192
Thr	Pro	Gly	Tyr	Ile	Tyr	Ser	Arg	Ile	Met	Asn	Pro	Thr	Asn	Asp	Val	
		50					55				60					
ttt	gaa	caa	aga	att	gct	gcc	ttg	gaa	ggg	ggg	att	ggg	gca	ttg	gcc	240
Phe	Glu	Gln	Arg	Ile	Ala	Ala	Leu	Glu	Gly	Gly	Ile	Gly	Ala	Leu	Ala	
65						70				75				80		
act	tct	tct	ggg	caa	tca	gct	caa	ttc	ttg	gcc	att	gct	ggg	ttg	gct	288
Thr	Ser	Ser	Gly	Gln	Ser	Ala	Gln	Phe	Leu	Ala	Ile	Ala	Gly	Leu	Ala	
				85					90					95		
cat	gct	ggg	gat	aac	att	atc	agt	aca	tcc	tac	ttg	tat	ggg	ggg	act	336
His	Ala	Gly	Asp	Asn	Ile	Ile	Ser	Thr	Ser	Tyr	Leu	Tyr	Gly	Gly	Thr	
			100					105					110			
tat	aat	caa	ttc	aaa	gtt	gct	ttc	aaa	cgt	ttg	ggc	att	gaa	acc	aaa	384
Tyr	Asn	Gln	Phe	Lys	Val	Ala	Phe	Lys	Arg	Leu	Gly	Ile	Glu	Thr	Lys	
		115					120					125				
ttc	gtt	aat	ggg	gac	gcc	gct	gaa	gat	ttt	gct	aaa	ttg	att	gac	gac	432
Phe	Val	Asn	Gly	Asp	Ala	Ala	Glu	Asp	Phe	Ala	Lys	Leu	Ile	Asp	Asp	
		130				135					140					
aag	aca	aaa	gct	att	tat	att	gaa	acc	att	gga	aac	cct	aaa	tat	aat	480
Lys	Thr	Lys	Ala	Ile	Tyr	Ile	Glu	Thr	Ile	Gly	Asn	Pro	Lys	Tyr	Asn	
145					150					155					160	
gtt	ccg	gac	ttt	gaa	aaa	atc	acc	aaa	ttg	gcc	cat	gaa	cac	ggg	att	528
Val	Pro	Asp	Phe	Glu	Lys	Ile	Thr	Lys	Leu	Ala	His	Glu	His	Gly	Ile	
				165					170					175		
cct	gtt	gtt	gtc	gac	aac	act	ttt	ggg	gct	ggg	gga	ttt	tta	gtt	aac	576
Pro	Val	Val	Val	Asp	Asn	Thr	Phe	Gly	Ala	Gly	Gly	Phe	Leu	Val	Asn	
			180					185					190			
cca	att	gcc	cac	ggg	gct	gat	att	gtt	gtt	cat	tct	gct	act	aaa	tgg	624
Pro	Ile	Ala	His	Gly	Ala	Asp	Ile	Val	Val	His	Ser	Ala	Thr	Lys	Trp	
		195				200						205				
att	ggg	ggg	cac	ggg	act	aca	att	gct	ggg	gtt	att	gtt	gat	tcc	ggg	672
Ile	Gly	Gly	His	Gly	Thr	Thr	Ile	Ala	Gly	Val	Ile	Val	Asp	Ser	Gly	
		210				215					220					
aac	ttc	cca	tgg	acc	gag	tac	cca	gaa	aaa	tac	cca	caa	ttc	tct	aaa	720
Asn	Phe	Pro	Trp	Thr	Glu	Tyr	Pro	Glu	Lys	Tyr	Pro	Gln	Phe	Ser	Lys	
225					230					235					240	
cca	tca	gaa	ggg	tac	cac	ggg	ttg	atc	ttg	aat	gat	gct	tta	ggg	aag	768
Pro	Ser	Glu	Gly	Tyr	His	Gly	Leu	Ile	Leu	Asn	Asp	Ala	Leu	Gly	Lys	
				245				250						255		

gcc gca tac att ggt cac ttg aga att gaa ttg ttg aga gac ttg ggt Ala Ala Tyr Ile Gly His Leu Arg Ile Glu Leu Leu Arg Asp Leu Gly 260 265 270	816
cca gct ttg aat cca ttt gga agt ttt ttg ttg ttg caa ggt tta gaa Pro Ala Leu Asn Pro Phe Gly Ser Phe Leu Leu Leu Gln Gly Leu Glu 275 280 285	864
act ttg tct ttg aga gtt gaa aga caa tct gaa aat gct ttg aaa ttg Thr Leu Ser Leu Arg Val Glu Arg Gln Ser Glu Asn Ala Leu Lys Leu 290 295 300	912
gcc caa tgg ttg gaa aag aac cca aat gtt gag tct gtg tcc tat ttg Ala Gln Trp Leu Glu Lys Asn Pro Asn Val Glu Ser Val Ser Tyr Leu 305 310 315 320	960
gga ttg cca tct cac gaa tcc cac gaa ttg agt aaa aaa tac ttg aac Gly Leu Pro Ser His Glu Ser His Glu Leu Ser Lys Lys Tyr Leu Asn 325 330 335	1008
aat gac gct aag tac ttt ggt ggt gct tta gca ttt act gtc aag gac Asn Asp Ala Lys Tyr Phe Gly Gly Ala Leu Ala Phe Thr Val Lys Asp 340 345 350	1056
atc acc aac acc tcc agc gac cca ttc aat gaa gcc tca cca aag ttg Ile Thr Asn Thr Ser Ser Asp Pro Phe Asn Glu Ala Ser Pro Lys Leu 355 360 365	1104
gtt gac aat ttg gag att gct tca aac ttg gct aat gtg ggt gac tct Val Asp Asn Leu Glu Ile Ala Ser Asn Leu Ala Asn Val Gly Asp Ser 370 375 380	1152
aag act ttg gtt att gct cca tgg ttt act aca cat caa caa ttg tct Lys Thr Leu Val Ile Ala Pro Trp Phe Thr Thr His Gln Gln Leu Ser 385 390 395 400	1200
gat gaa gaa aag ttg gct tct ggt gtt acc aag ggc tta atc aga gtt Asp Glu Glu Lys Leu Ala Ser Gly Val Thr Lys Gly Leu Ile Arg Val 405 410 415	1248
tct act ggt act gaa tat att gat gat att att aac gac ttt gaa caa Ser Thr Gly Thr Glu Tyr Ile Asp Asp Ile Ile Asn Asp Phe Glu Gln 420 425 430	1296
gca ttc aag aag gtt tat aac aac taa Ala Phe Lys Lys Val Tyr Asn Asn 435 440	1323

<210> 52

<211> 440

<212> PRT

<213> Candida albicans

<400> 52

Met Pro Ser His Phe Asp Thr Leu Gln Leu His Ala Gly Gln Pro Val
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Glu Lys Pro His Gln Pro Arg Ala Pro Pro Ile Tyr Ala Thr Thr Ser
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Tyr Val Phe Asn Asp Ser Lys His Gly Ala Gln Leu Phe Gly Leu Glu
35 40 45

Thr Pro Gly Tyr Ile Tyr Ser Arg Ile Met Asn Pro Thr Asn Asp Val
50 55 60

Phe Glu Gln Arg Ile Ala Ala Leu Glu Gly Gly Ile Gly Ala Leu Ala
65 70 75 80

Thr Ser Ser Gly Gln Ser Ala Gln Phe Leu Ala Ile Ala Gly Leu Ala
85 90 95

His Ala Gly Asp Asn Ile Ile Ser Thr Ser Tyr Leu Tyr Gly Gly Thr
100 105 110

Tyr Asn Gln Phe Lys Val Ala Phe Lys Arg Leu Gly Ile Glu Thr Lys
115 120 125

Phe Val Asn Gly Asp Ala Ala Glu Asp Phe Ala Lys Leu Ile Asp Asp
130 135 140

Lys Thr Lys Ala Ile Tyr Ile Glu Thr Ile Gly Asn Pro Lys Tyr Asn
145 150 155 160

Val Pro Asp Phe Glu Lys Ile Thr Lys Leu Ala His Glu His Gly Ile
165 170 175

Pro Val Val Val Asp Asn Thr Phe Gly Ala Gly Gly Phe Leu Val Asn
180 185 190

Pro Ile Ala His Gly Ala Asp Ile Val Val His Ser Ala Thr Lys Trp
195 200 205

Ile Gly Gly His Gly Thr Thr Ile Ala Gly Val Ile Val Asp Ser Gly
210 215 220

Asn Phe Pro Trp Thr Glu Tyr Pro Glu Lys Tyr Pro Gln Phe Ser Lys
225 230 235 240

Pro Ser Glu Gly Tyr His Gly Leu Ile Leu Asn Asp Ala Leu Gly Lys
 245 250 255

Ala Ala Tyr Ile Gly His Leu Arg Ile Glu Leu Leu Arg Asp Leu Gly
 260 265 270

Pro Ala Leu Asn Pro Phe Gly Ser Phe Leu Leu Leu Gln Gly Leu Glu
 275 280 285

Thr Leu Ser Leu Arg Val Glu Arg Gln Ser Glu Asn Ala Leu Lys Leu
 290 295 300

Ala Gln Trp Leu Glu Lys Asn Pro Asn Val Glu Ser Val Ser Tyr Leu
 305 310 315 320

Gly Leu Pro Ser His Glu Ser His Glu Leu Ser Lys Lys Tyr Leu Asn
 325 330 335

Asn Asp Ala Lys Tyr Phe Gly Gly Ala Leu Ala Phe Thr Val Lys Asp
 340 345 350

Ile Thr Asn Thr Ser Ser Asp Pro Phe Asn Glu Ala Ser Pro Lys Leu
 355 360 365

Val Asp Asn Leu Glu Ile Ala Ser Asn Leu Ala Asn Val Gly Asp Ser
 370 375 380

Lys Thr Leu Val Ile Ala Pro Trp Phe Thr Thr His Gln Gln Leu Ser
 385 390 395 400

Asp Glu Glu Lys Leu Ala Ser Gly Val Thr Lys Gly Leu Ile Arg Val
 405 410 415

Ser Thr Gly Thr Glu Tyr Ile Asp Asp Ile Ile Asn Asp Phe Glu Gln
 420 425 430

Ala Phe Lys Lys Val Tyr Asn Asn
 435 440

<210> 53

<211> 1290

<212> DNA

<213> Schizosaccharomyces pombe

<220>

<221> CDS

<222> (1)..(1290)

<400> 53

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caa gag cct gat gct gct acc agc tct cgt gcc gtt ccc atc tac gct	96
Gln Glu Pro Asp Ala Ala Thr Ser Ser Arg Ala Val Pro Ile Tyr Ala	
20 25 30	
act act tcc tat gtt ttc cgt gat tgc gac cat ggc ggc cgc ttg ttc	144
Thr Thr Ser Tyr Val Phe Arg Asp Cys Asp His Gly Gly Arg Leu Phe	
35 40 45	
gga tta cag gaa cca ggt tac atc tac tcg cgt atg atg aat ccc acc	192
Gly Leu Gln Glu Pro Gly Tyr Ile Tyr Ser Arg Met Met Asn Pro Thr	
50 55 60	
gcc gac gtt ttt gag aaa cgt att gcc gcc ttg gag cat ggc gct gct	240
Ala Asp Val Phe Glu Lys Arg Ile Ala Ala Leu Glu His Gly Ala Ala	
65 70 75 80	
gca atc gct act agt tcc ggt act tcc gct ctc ttc atg gct ttg acc	288
Ala Ile Ala Thr Ser Ser Gly Thr Ser Ala Leu Phe Met Ala Leu Thr	
85 90 95	
acg ttg gct aag gcc ggt gat aac att gtc tcc act tct tac ctt tat	336
Thr Leu Ala Lys Ala Gly Asp Asn Ile Val Ser Thr Ser Tyr Leu Tyr	
100 105 110	
ggt ggt act tac aac ctc ttc aag gtt acc ctg cct aga ttg gga att	384
Gly Gly Thr Tyr Asn Leu Phe Lys Val Thr Leu Pro Arg Leu Gly Ile	
115 120 125	
act acc aag ttt gtc aat ggt gat gat cct aat gat ctt gca gct cag	432
Thr Thr Lys Phe Val Asn Gly Asp Asp Pro Asn Asp Leu Ala Ala Gln	
130 135 140	
att gat gaa aac aca aag gct gtt tac gtt gag tcc atc ggc aat ccc	480
Ile Asp Glu Asn Thr Lys Ala Val Tyr Val Glu Ser Ile Gly Asn Pro	
145 150 155 160	
atg tac aac gtt ccc gat ttt gag cgt atc gct gag gtt gct cat gcc	528
Met Tyr Asn Val Pro Asp Phe Glu Arg Ile Ala Glu Val Ala His Ala	
165 170 175	
gct ggt gtg cct tta atg gtc gat aac act ttt ggc ggc ggt ggt tat	576
Ala Gly Val Pro Leu Met Val Asp Asn Thr Phe Gly Gly Gly Gly Tyr	
180 185 190	

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act aag tgg atc ggt ggt cat ggc act act att ggc ggt gtg att gtt Thr Lys Trp Ile Gly Gly His Gly Thr Thr Ile Gly Gly Val Ile Val 210 215 220	672
gat agt ggt aag ttt gac tgg aag aag aac agc aag cgt ttc cct gaa Asp Ser Gly Lys Phe Asp Trp Lys Lys Asn Ser Lys Arg Phe Pro Glu 225 230 235 240	720
ttc aac gag cct cat ccc ggt tac cat ggc atg gtc ttt act gaa act Phe Asn Glu Pro His Pro Gly Tyr His Gly Met Val Phe Thr Glu Thr 245 250 255	768
ttt ggt aac ttg gca tat gct ttt gct tgc cgt act caa act ctc cgt Phe Gly Asn Leu Ala Tyr Ala Phe Ala Cys Arg Thr Gln Thr Leu Arg 260 265 270	816
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tct tac cct ggt ctt gaa tct cac gtc tct cac aaa ctt gcc aag aag Ser Tyr Pro Gly Leu Glu Ser His Val Ser His Lys Leu Ala Lys Lys 325 330 335	1008
tac ttg aaa aat ggt tac ggc gcc gtt ctc agc ttt ggc gct aaa ggt Tyr Leu Lys Asn Gly Tyr Gly Ala Val Leu Ser Phe Gly Ala Lys Gly 340 345 350	1056
ggc cct gat caa agt cgt aag gta gtc aat gcc tta aag ctt gct agt Gly Pro Asp Gln Ser Arg Lys Val Val Asn Ala Leu Lys Leu Ala Ser 355 360 365	1104
cag ttg gcc aat gtt ggt gat gcc aaa act ttg gtt atc gct cct gcc Gln Leu Ala Asn Val Gly Asp Ala Lys Thr Leu Val Ile Ala Pro Ala 370 375 380	1152
tat acc act cat tta caa tta act gat gag gag caa att tct gcc ggt Tyr Thr Thr His Leu Gln Leu Thr Asp Glu Glu Gln Ile Ser Ala Gly 385 390 395 400	1200
gtc act aag gat ctt att cgt gtg gcc gtc ggt att gag cac atc gat Val Thr Lys Asp Leu Ile Arg Val Ala Val Gly Ile Glu His Ile Asp 405 410 415	1248
gat att atc gcc gac ttt gct caa gct ttg gaa gtt gcc taa Asp Ile Ile Ala Asp Phe Ala Gln Ala Leu Glu Val Ala 420 425	1290

<210> 54

<211> 429

<212> PRT

<213> Schizosaccharomyces pombe

<400> 54

Met Pro Val Glu Ser Glu His Phe Glu Thr Leu Gln Leu His Ala Gly
1 5 10 15

Gln Glu Pro Asp Ala Ala Thr Ser Ser Arg Ala Val Pro Ile Tyr Ala
20 25 30

Thr Thr Ser Tyr Val Phe Arg Asp Cys Asp His Gly Gly Arg Leu Phe
35 40 45

Gly Leu Gln Glu Pro Gly Tyr Ile Tyr Ser Arg Met Met Asn Pro Thr
50 55 60

Ala Asp Val Phe Glu Lys Arg Ile Ala Ala Leu Glu His Gly Ala Ala
65 70 75 80

Ala Ile Ala Thr Ser Ser Gly Thr Ser Ala Leu Phe Met Ala Leu Thr
85 90 95

Thr Leu Ala Lys Ala Gly Asp Asn Ile Val Ser Thr Ser Tyr Leu Tyr
100 105 110

Gly Gly Thr Tyr Asn Leu Phe Lys Val Thr Leu Pro Arg Leu Gly Ile
115 120 125

Thr Thr Lys Phe Val Asn Gly Asp Asp Pro Asn Asp Leu Ala Ala Gln
130 135 140

Ile Asp Glu Asn Thr Lys Ala Val Tyr Val Glu Ser Ile Gly Asn Pro
145 150 155 160

Met Tyr Asn Val Pro Asp Phe Glu Arg Ile Ala Glu Val Ala His Ala
165 170 175

Ala Gly Val Pro Leu Met Val Asp Asn Thr Phe Gly Gly Gly Gly Tyr
180 185 190

Leu Val Arg Pro Ile Asp His Gly Ala Asp Ile Val Thr His Ser Ala
 195 200 205

Thr Lys Trp Ile Gly Gly His Gly Thr Thr Ile Gly Gly Val Ile Val
 210 215 220

Asp Ser Gly Lys Phe Asp Trp Lys Lys Asn Ser Lys Arg Phe Pro Glu
 225 230 235 240

Phe Asn Glu Pro His Pro Gly Tyr His Gly Met Val Phe Thr Glu Thr
 245 250 255

Phe Gly Asn Leu Ala Tyr Ala Phe Ala Cys Arg Thr Gln Thr Leu Arg
 260 265 270

Asp Val Gly Gly Asn Ala Asn Pro Phe Gly Val Phe Leu Leu Leu Gln
 275 280 285

Gly Leu Glu Thr Leu Ser Leu Arg Met Glu Arg His Val Gln Asn Ala
 290 295 300

Phe Ala Leu Ala Lys Tyr Leu Glu Lys His Pro Lys Val Asn Trp Val
 305 310 315 320

Ser Tyr Pro Gly Leu Glu Ser His Val Ser His Lys Leu Ala Lys Lys
 325 330 335

Tyr Leu Lys Asn Gly Tyr Gly Ala Val Leu Ser Phe Gly Ala Lys Gly
 340 345 350

Gly Pro Asp Gln Ser Arg Lys Val Val Asn Ala Leu Lys Leu Ala Ser
 355 360 365

Gln Leu Ala Asn Val Gly Asp Ala Lys Thr Leu Val Ile Ala Pro Ala
 370 375 380

Tyr Thr Thr His Leu Gln Leu Thr Asp Glu Glu Gln Ile Ser Ala Gly
 385 390 395 400

Val Thr Lys Asp Leu Ile Arg Val Ala Val Gly Ile Glu His Ile Asp
 405 410 415

Asp Ile Ile Ala Asp Phe Ala Gln Ala Leu Glu Val Ala
 420 425

<210> 55
 <211> 52
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:PCR primer

<400> 55
 cccgggatcc gctagcggcg cgccggccgg cccggtgtga aataccgcac ag 52

<210> 56
 <211> 53
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:PCR primer

<400> 56
 tctagactcg agcggcccgcg gccggccttt aaattgaaga cgaaagggcc tcg 53

<210> 57
 <211> 47
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:PCR primer

<400> 57
 gagatctaga cccggggatc cgctagcggg ctgctaaagg aagcgga 47

<210> 58
 <211> 38
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:PCR primer

<400> 58
 gagaggcgcg ccgctagcgt gggcgaagaa ctccagca 38

<210> 59
 <211> 34
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:PCR primer

<400> 59
 gagaggcgcg ccgcgcaaag tcccgttcg tgaa 34

<210> 60
 <211> 34
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:PCR primer

<400> 60
 gagagggcgg ccgctcaagt cggtaagcc acgc 34

<210> 61
 <211> 140
 <212> DNA
 <213> Artificial sequence

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 <223> Description of the artificial sequence:PCR primer

<400> 61
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 tctagaccog ggatttaa 140

<210> 62
 <211> 140
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:PCR primer

<400> 62
 gatcatttaa atcccgggtc tagaggatcc caattgttaa ttaacgcaga agagcatcga 60
 tgtcgacgat atccctaggt ccgaactagt catatgacgc gtggtaccgg gcccgacgtc 120
 aggcctctcg agatttaa 140

<210> 63
 <211> 33
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:PCR primer

<400> 63
 gagagcggcc gccgatcctt ttaacccat cac 33

<210> 64
 <211> 32
 <212> DNA
 <213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR primer

<400> 64

aggagcggcc gccatcggca ttttcttttg cg

32

<210> 65

<211> 5091

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:plasmid

<400> 65

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```

<210> 66

<211> 4323

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: plasmid

<400> 66

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```

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```

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gatgtgcttt tgccatagta tgctttgtta aataaagatt cttegcttg gtagccatct 4260
tcagttccag tgtttgcttc aaatactaag tatttggtgc ctttatcttc tacgtagtga 4320
gga                                         4323

```

```

<210> 67
<211> 35
<212> DNA
<213> Artificial sequence

```

```

<220>
<223> Description of the artificial sequence: PCR primer

```

```

<400> 67
gagagagaga cgcgtcccag tggctgagac gcatc                                         35

```

```

<210> 68
<211> 34
<212> DNA
<213> Artificial sequence

```

```

<220>
<223> Description of the artificial sequence: PCR primer

```

```

<400> 68
ctctctctgt cgacgaattc aatcttacgg cctg                                         34

```

```

<210> 69
<211> 5860
<212> DNA
<213> Artificial sequence

```

```

<220>
<223> Description of the artificial sequence: plasmid

```

```

<400> 69
cccggtagca cgcgtcccag tggctgagac gcatccgcta aagccccagg aaccctgtgc      60
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aactgtcagc acgtagatcg aaaggtgcac aaaggtggcc ctggctcgta agaaatatgg      180
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```


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<210> 70
 <211> 38
 <212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: PCR primer

<400> 70

cggcaccacc gacatcatct tcacctgccc tcgttccg 38

<210> 71

<211> 38

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: PCR primer

<400> 71

cggaacgagg gcaggtgaag atgatgtcgg tgggtgccg 38

<210> 72

<211> 1266

<212> DNA

<213> LysC mutant

<220>

<221> CDS

<222> (1)..(1266)

<400> 72

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1 5 10 15

gaa cgc att aga aac gtc gct gaa cgg atc gtt gcc acc aag aag gct 96
Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala
20 25 30

gga aat gat gtc gtg gtt gtc tgc tcc gca atg gga gac acc acg gat 144
Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp
35 40 45

gaa ctt cta gaa ctt gca gcg gca gtg aat ccc gtt ccg cca gct cgt 192
Glu Leu Leu Glu Leu Ala Ala Val Asn Pro Val Pro Pro Ala Arg
50 55 60

gaa atg gat atg ctc ctg act gct ggt gag cgt att tct aac gct ctc 240
Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu
65 70 75 80

gtc gcc atg gct att gag tcc ctt ggc gca gaa gcc caa tct ttc acg 288
Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr
85 90 95

ggc tct cag gct ggt gtg ctc acc acc gag cgc cac gga aac gca cgc 336
Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg
100 105 110

att gtt gat gtc act cca ggt cgt gtg cgt gaa gca ctc gat gag ggc 384

Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly	
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Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg	
130 135 140	
gat gtc acc acg ttg ggt cgt ggt ggt tct gac acc act gca gtt gcg	480
Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala	
145 150 155 160	
ttg gca gct gct ttg aac gct gat gtg tgt gag att tac tcg gac gtt	528
Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val	
165 170 175	
gac ggt gtg tat acc gct gac ccg cgc atc gtt cct aat gca cag aag	576
Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys	
180 185 190	
ctg gaa aag ctc agc ttc gaa gaa atg ctg gaa ctt gct gct gtt ggc	624
Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly	
195 200 205	
tcc aag att ttg gtg ctg cgc agt gtt gaa tac gct cgt gca ttc aat	672
Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn	
210 215 220	
gtg cca ctt cgc gta cgc tcg tct tat agt aat gat ccc ggc act ttg	720
Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu	
225 230 235 240	
att gcc ggc tct atg gag gat att cct gtg gaa gaa gca gtc ctt acc	768
Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr	
245 250 255	
ggt gtc gca acc gac aag tcc gaa gcc aaa gta acc gtt ctg ggt att	816
Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile	
260 265 270	
tcc gat aag cca ggc gag gct gcg aag gtt ttc cgt gcg ttg gct gat	864
Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp	
275 280 285	
gca gaa atc aac att gac atg gtt ctg cag aac gtc tct tct gta gaa	912
Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu	
290 295 300	
gac ggc acc acc gac atc atc ttc acc tgc cct cgt tcc gac ggc cgc	960
Asp Gly Thr Thr Asp Ile Ile Phe Thr Cys Pro Arg Ser Asp Gly Arg	
305 310 315 320	
cgc gcg atg gag atc ttg aag aag ctt cag gtt cag ggc aac tgg acc	1008
Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr	
325 330 335	
aat gtg ctt tac gac gac cag gtc ggc aaa gtc tcc ctc gtg ggt gct	1056
Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala	
340 345 350	
ggc atg aag tct cac cca ggt gtt acc gca gag ttc atg gaa gct ctg	1104

Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu
 355 360 365

cgc gat gtc aac gtg aac atc gaa ttg att tcc acc tct gag att cgt 1152
 Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg
 370 375 380

att tcc gtg ctg atc cgt gaa gat gat ctg gat gct gct gca cgt gca 1200
 Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala
 385 390 395 400

ttg cat gag cag ttc cag ctg ggc ggc gaa gac gaa gcc gtc gtt tat 1248
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 405 410 415

gca ggc acc gga cgc taa 1266
 Ala Gly Thr Gly Arg
 420

<210> 73
 <211> 421
 <212> PRT
 <213> LysC mutant

<400> 73

Val Ala Leu Val Val Gln Lys Tyr Gly Gly Ser Ser Leu Glu Ser Ala
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Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp
 35 40 45

Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg
 50 55 60

Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu
 65 70 75 80

Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr
 85 90 95

Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg
 100 105 110

Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly
 115 120 125

Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg

130

135

140

Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala
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Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val
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Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys
 180 185 190

Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly
 195 200 205

Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn
 210 215 220

Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu
 225 230 235 240

Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr
 245 250 255

Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile
 260 265 270

Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp
 275 280 285

Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu
 290 295 300

Asp Gly Thr Thr Asp Ile Ile Phe Thr Cys Pro Arg Ser Asp Gly Arg
 305 310 315 320

Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr
 325 330 335

Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala
 340 345 350

Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu
 355 360 365

Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg

370

375

380

Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala
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Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr
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Ala Gly Thr Gly Arg
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<210> 74
 <211> 5860
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence: plasmid

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<210> 75
 <211> 31
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence: PCR primer

<400> 75
 gagaggatcc ggaaggtgaa tcgaatttcg g 31

<210> 76
 <211> 40
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence: PCR primer

<400> 76
ctatttgctgt cggcgctcat gattctccaa aaataatcgc 40

<210> 77
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: PCR primer

<400> 77
atgagcgccg acagcaatag 20

<210> 78
<211> 29
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: PCR primer

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gaactctaga tcagaacgcc gccacggac 29

<210> 79
<211> 6591
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: plasmid

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